

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
31 July 2003 (31.07.2003)

PCT

(10) International Publication Number  
**WO 03/062379 A2**

(51) International Patent Classification<sup>7</sup>: C12N  
(21) International Application Number: PCT/US03/01363  
(22) International Filing Date: 14 January 2003 (14.01.2003)  
(25) Filing Language: English  
(26) Publication Language: English  
(30) Priority Data:  
60/349,946 17 January 2002 (17.01.2002) US  
60/349,413 17 January 2002 (17.01.2002) US

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: MOLECULES FOR DISEASE DETECTION AND TREATMENT

(57) Abstract: The present invention provides purified disease detection and treatment molecule polynucleotides (mddt). Also encompassed are the polypeptides (MDDT) encoded by mddt. The invention also provides for the use of mddt, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing mddt for the expression of MDDT. The invention additionally provides for the use of isolated and purified MDDT to induce antibodies and to screen libraries of compounds and the use of anti-MDDT antibodies in diagnostic assays. Also provided are microarrays containing mddt and methods of use.

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## TECHNICAL FIELD

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DNA-based arrays can provide a simple way to explore the expression of a single polymorphic gene or a large number of genes. When the expression of a single gene is explored, DNA-based arrays are employed to detect the expression of specific gene variants. For example, a p53 tumor suppressor gene array is used to determine whether individuals are carrying mutations that predispose them to cancer. A cytochrome p450 gene array is useful to determine whether individuals have one of a number of specific mutations that could result in increased drug metabolism, drug resistance or drug toxicity.

DNA-based array technology is especially relevant for the rapid screening of expression of a large number of genes. There is a growing awareness that gene expression is affected in a global fashion. A genetic predisposition, disease or therapeutic treatment may affect, directly or indirectly, the expression of a large number of genes. In some cases the interactions may be expected, such as when the genes are part of the same signaling pathway. In other cases, such as when the genes participate in separate signaling pathways, the interactions may be totally unexpected. Therefore, DNA-based arrays can be used to investigate how genetic predisposition, disease, or therapeutic treatment affects the expression of a large number of genes.

The discovery of new molecules for disease detection and treatment satisfies a need in the art by providing new compositions which are useful in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, the expression of molecules for disease detection and treatment.

## SUMMARY OF THE INVENTION

The present invention relates to human disease detection and treatment molecule polynucleotides (mddt) as presented in the Sequence Listing. The mddt uniquely identify genes encoding structural, functional, and regulatory disease detection and treatment molecules.

The invention provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In one alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104. In another alternative, the polynucleotide comprises at least 30 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide

sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In another alternative, the polynucleotide comprises at least 60 contiguous nucleotides of a

5 polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the

10 polynucleotide of b); and e) an RNA equivalent of a) through d). The invention further provides a composition for the detection of expression of disease detection and treatment molecule polynucleotides comprising at least one isolated polynucleotide comprising a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring

15 polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d); and a detectable label.

The invention also provides a method for detecting a target polynucleotide in a sample, said

20 target polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide

25 of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention also provides a method for detecting a target polynucleotide in a sample, said

30 target polynucleotide having a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary

35 to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a)

hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof. In one alternative, the invention provides a composition comprising a target polynucleotide of the method, wherein said probe comprises at least 30 contiguous nucleotides. In one alternative, the invention provides a composition comprising a target polynucleotide of the method, wherein said probe comprises at least 60 contiguous nucleotides.

10 The invention further provides a recombinant polynucleotide comprising a promoter sequence operably linked to an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; 15 c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a disease detection and treatment molecule polypeptide, the method comprising a) culturing a cell under conditions suitable for expression of the disease detection and treatment molecule polypeptide, wherein said cell is transformed with a recombinant polynucleotide, said recombinant polynucleotide comprising an isolated polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; ii) a 25 polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and b) recovering the disease detection and treatment molecule polypeptide so expressed. The invention additionally provides a 30 method wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

The invention also provides an isolated disease detection and treatment molecule polypeptide (MDDT) encoded by at least one polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104. The invention further provides a method of screening for 35 a test compound that specifically binds to the polypeptide having an amino acid sequence selected

from the group consisting of SEQ ID NO:105-208. The method comprises a) combining the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208 with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208 to the test compound, thereby identifying a compound that specifically binds to the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

The invention further provides a microarray wherein at least one element of the microarray is an isolated polynucleotide comprising at least 30 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The invention also provides a method for generating a transcript image of a sample which contains polynucleotides. The method comprises a) labeling the polynucleotides of the sample, b) contacting the elements of the microarray with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and c) quantifying the expression of the polynucleotides in the sample.

Additionally, the invention provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence, at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) exposing a sample comprising the target polynucleotide to a compound, b) detecting altered expression of the target polynucleotide, and c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a

polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and alternatively, the target polynucleotide comprises a polynucleotide sequence of a fragment of a polynucleotide selected from the group consisting of i-v above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

The invention further provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. In one alternative, the invention provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. In one alternative, the polynucleotide encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. In another alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID

NO:1-104.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

10 The invention further provides a composition comprising a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence  
15 selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. The invention additionally provides a method of treating a disease or condition associated with  
20 decreased expression of functional MDDT, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide  
25 comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. The method comprises a) exposing a  
30 sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional MDDT, comprising administering to a patient in need of such treatment the composition.

35 Additionally, the invention provides a method for screening a compound for effectiveness as

an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional MDDT, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

### DESCRIPTION OF THE TABLES

Table 1 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with the sequence identification numbers (SEQ ID NO:s) and open reading frame identification numbers (ORF IDs) corresponding to polypeptides encoded by the template ID.

Table 2 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with their GenBank hits (GI Numbers), probability scores, and functional annotations

corresponding to the GenBank hits.

Table 3 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated “start” and “stop” nucleotide positions. The reading frames of the polynucleotide segments and the Pfam hits, Pfam descriptions, and E-values corresponding to the polypeptide domains encoded by the polynucleotide segments are indicated.

Table 4 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated “start” and “stop” nucleotide positions. The reading frames of the polynucleotide segments are shown, and the polypeptides encoded by the polynucleotide segments constitute either signal peptide (SP) or transmembrane (TM) domains, as indicated. For TM domains, the membrane topology of the encoded polypeptide sequence is indicated as being transmembrane or on the cytosolic or non-cytosolic side of the cell membrane or organelle.

Table 5 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with the component sequence identification spans (component spans) corresponding to each template. The component sequences, which were used to assemble the template sequences, are defined by the spans indicating the nucleotide positions along each template.

Table 6 shows the tissue distribution profiles for the templates of the invention.

Table 7 shows the sequence identification numbers (SEQ ID NO:s) corresponding to the polypeptides of the present invention, along with the reading frames used to obtain the polypeptide segments, the lengths of the polypeptide segments, the “start” and “stop” nucleotide positions of the polynucleotide sequences used to define the encoded polypeptide segments, the GenBank hits (GI Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

Table 8 summarizes the bioinformatics tools which are useful for analysis of the polynucleotides of the present invention. The first column of Table 8 lists analytical tools, programs, and algorithms, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences).

## **DETAILED DESCRIPTION OF THE INVENTION**



Before the nucleic acid sequences and methods are presented, it is to be understood that this invention is not limited to the particular machines, methods, and materials described. Although particular embodiments are described, machines, methods, and materials similar or equivalent to these embodiments may be used to practice the invention. The preferred machines, methods, and materials set forth are not intended to limit the scope of the invention which is limited only by the appended claims.

The singular forms “a”, “an”, and “the” include plural reference unless the context clearly dictates otherwise. All technical and scientific terms have the meanings commonly understood by one of ordinary skill in the art. All publications are incorporated by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are presented and which might be used in connection with the invention. Nothing in the specification is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

### **Definitions**

As used herein, the lower case “mddt” refers to a nucleic acid sequence, while the upper case “MDDT” refers to an amino acid sequence encoded by mddt. A “full-length” mddt refers to a nucleic acid sequence containing the entire coding region of a gene endogenously expressed in human tissue.

“Adjuvants” are materials such as Freund's adjuvant, mineral gels (aluminum hydroxide), and surface active substances (lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol) which may be administered to increase a host's immunological response.

“Allele” refers to an alternative form of a nucleic acid sequence. Alleles result from a “mutation,” a change or an alternative reading of the genetic code. Any given gene may have none, one, or many allelic forms. Mutations which give rise to alleles include deletions, additions, or substitutions of nucleotides. Each of these changes may occur alone, or in combination with the others, one or more times in a given nucleic acid sequence. The present invention encompasses allelic mddt.

An “allelic variant” is an alternative form of the gene encoding MDDT. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of

nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

“Altered” nucleic acid sequences encoding MDDT include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as MDDT or a polypeptide with at least one functional characteristic of MDDT. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding MDDT, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding MDDT. The encoded protein may also be “altered,” and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent MDDT. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of MDDT is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

“Amino acid sequence” refers to a peptide, a polypeptide, or a protein of either natural or synthetic origin. The amino acid sequence is not limited to the complete, endogenous amino acid sequence and may be a fragment, epitope, variant, or derivative of a protein expressed by a nucleic acid sequence.

“Amplification” refers to the production of additional copies of a sequence and is carried out using polymerase chain reaction (PCR) technologies well known in the art.

“Antibody” refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')<sub>2</sub>, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind MDDT polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term “aptamer” refers to a nucleic acid or oligonucleotide molecule that binds to a specific molecular target. Aptamers are derived from an in vitro evolutionary process (e.g., SELEX (Systematic Evolution of Ligands by EXponential Enrichment), described in U.S. Patent No.

5,270,163), which selects for target-specific aptamer sequences from large combinatorial libraries. Aptamer compositions may be double-stranded or single-stranded, and may include deoxyribonucleotides, ribonucleotides, nucleotide derivatives, or other nucleotide-like molecules. The nucleotide components of an aptamer may have modified sugar groups (e.g., the 2'-OH group of a ribonucleotide may be replaced by 2'-F or 2'-NH<sub>2</sub>), which may improve a desired property, e.g., resistance to nucleases or longer lifetime in blood. Aptamers may be conjugated to other molecules, e.g., a high molecular weight carrier to slow clearance of the aptamer from the circulatory system. Aptamers may be specifically cross-linked to their cognate ligands, e.g., by photo-activation of a cross-linker. (See, e.g., Brody, E.N. and L. Gold (2000) J. Biotechnol. 74:5-13.)

The term "intramer" refers to an aptamer which is expressed in vivo. For example, a vaccinia virus-based RNA expression system has been used to express specific RNA aptamers at high levels in the cytoplasm of leukocytes (Blind, M. et al. (1999) Proc. Natl Acad. Sci. USA 96:3606-3610).

The term "spiegelmer" refers to an aptamer which includes L-DNA, L-RNA, or other left-handed nucleotide derivatives or nucleotide-like molecules. Aptamers containing left-handed nucleotides are resistant to degradation by naturally occurring enzymes, which normally act on substrates containing right-handed nucleotides.

"Antisense sequence" refers to a sequence capable of specifically hybridizing to a target sequence. The antisense sequence may include DNA, RNA, or any nucleic acid mimic or analog such as peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine.

"Antisense technology" refers to any technology which relies on the specific hybridization of an antisense sequence to a target sequence.

A "bin" is a portion of computer memory space used by a computer program for storage of data, and bounded in such a manner that data stored in a bin may be retrieved by the program.

"Biologically active" refers to an amino acid sequence having a structural, regulatory, or biochemical function of a naturally occurring amino acid sequence.

"Clone joining" is a process for combining gene bins based upon the bins' containing sequence information from the same clone. The sequences may assemble into a primary gene transcript as well as one or more splice variants.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing (5'-A-G-T-3' pairs with its complement 3'-T-C-A-5').

A "component sequence" is a nucleic acid sequence selected by a computer program such as PHRED and used to assemble a consensus or template sequence from one or more component sequences.

A "consensus sequence" or "template sequence" is a nucleic acid sequence which has been assembled from overlapping sequences, using a computer program for fragment assembly such as the GELVIEW fragment assembly system (Genetics Computer Group (GCG), Madison WI) or using a relational database management system (RDMS).

"Conservative amino acid substitutions" are those substitutions that, when made, least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions.

	Original Residue	Conservative Substitution
15	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
20	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
25	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
30	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr

35

Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

"Deletion" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or amino acid residue, respectively, is absent.

"Derivative" refers to the chemical modification of a nucleic acid sequence, such as by replacement of hydrogen by an alkyl, acyl, amino, hydroxyl, or other group.

"Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

5 The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of MDDT. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of MDDT.

10 "E-value" refers to the statistical probability that a match between two sequences occurred by chance.

"Exon shuffling" refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be assembled through the novel reassortment of stable substructures, thus allowing acceleration of the evolution of new protein functions.

15 A "fragment" is a unique portion of mddt or MDDT which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 10 to 1000 contiguous amino acid residues or nucleotides. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous amino acid residues or nucleotides in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing and the figures, may be encompassed by the present embodiments.

25 A fragment of mddt comprises a region of unique polynucleotide sequence that specifically identifies mddt, for example, as distinct from any other sequence in the same genome. A fragment of mddt is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish mddt from related polynucleotide sequences. The precise length of a fragment of mddt and the region of mddt to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

30 A fragment of MDDT is encoded by a fragment of mddt. A fragment of MDDT comprises a region of unique amino acid sequence that specifically identifies MDDT. For example, a fragment of MDDT is useful as an immunogenic peptide for the development of antibodies that specifically

recognize MDDT. The precise length of a fragment of MDDT and the region of MDDT to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" nucleotide sequence is one containing at least a start site for translation to a protein sequence, followed by an open reading frame and a stop site, and encoding a "full length" polypeptide.

"Hit" refers to a sequence whose annotation will be used to describe a given template. Criteria for selecting the top hit are as follows: if the template has one or more exact nucleic acid matches, the top hit is the exact match with highest percent identity. If the template has no exact matches but has significant protein hits, the top hit is the protein hit with the lowest E-value. If the template has no significant protein hits, but does have significant non-exact nucleotide hits, the top hit is the nucleotide hit with the lowest E-value.

"Homology" refers to sequence similarity either between a reference nucleic acid sequence and at least a fragment of an mddt or between a reference amino acid sequence and a fragment of an MDDT.

"Hybridization" refers to the process by which a strand of nucleotides anneals with a complementary strand through base pairing. Specific hybridization is an indication that two nucleic acid sequences share a high degree of identity. Specific hybridization complexes form under defined annealing conditions, and remain hybridized after the "washing" step. The defined hybridization conditions include the annealing conditions and the washing step(s), the latter of which is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid probes that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency.

Generally, stringency of hybridization is expressed with reference to the temperature under which the wash step is carried out. Generally, such wash temperatures are selected to be about 5°C to 20°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating  $T_m$  and conditions for nucleic acid hybridization is well known and can be found in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS,

for 1 hour. Alternatively, temperatures of about 65°C, 60°C, or 55°C may be used. SSC concentration may be varied from about 0.2 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, denatured salmon sperm DNA at about 100-200 µg/ml. Useful variations on these conditions will be readily apparent to those skilled in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their resultant proteins.

Other parameters, such as temperature, salt concentration, and detergent concentration may be varied to achieve the desired stringency. Denaturants, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as RNA:DNA hybridizations. Appropriate hybridization conditions are routinely determinable by one of ordinary skill in the art.

“Immunologically active” or “immunogenic” describes the potential for a natural, recombinant, or synthetic peptide, epitope, polypeptide, or protein to induce antibody production in appropriate animals, cells, or cell lines.

“Immune response” can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An “immunogenic fragment” is a polypeptide or oligopeptide fragment of MDDT which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term “immunogenic fragment” also includes any polypeptide or oligopeptide fragment of MDDT which can be useful in any of the antibody production methods disclosed herein or known in the art.

“Insertion” or “addition” refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or residue, respectively, is added to the sequence.

“Labeling” refers to the covalent or noncovalent joining of a polynucleotide, polypeptide, or antibody with a reporter molecule capable of producing a detectable or measurable signal.

“Microarray” is any arrangement of nucleic acids, amino acids, antibodies, etc., on a substrate. The substrate may be a solid support such as beads, glass, paper, nitrocellulose, nylon, or an appropriate membrane.

“Linkers” are short stretches of nucleotide sequence which may be added to a vector or an mddt to create restriction endonuclease sites to facilitate cloning. “Polylinkers” are engineered to incorporate multiple restriction enzyme sites and to provide for the use of enzymes which leave 5' or 3' overhangs (e.g., BamHI, EcoRI, and HindIII) and those which provide blunt ends (e.g., EcoRV,

SnaBI, and StuI).

“Naturally occurring” refers to an endogenous polynucleotide or polypeptide that may be isolated from viruses or prokaryotic or eukaryotic cells.

“Nucleic acid sequence” refers to the specific order of nucleotides joined by phosphodiester bonds in a linear, polymeric arrangement. Depending on the number of nucleotides, the nucleic acid sequence can be considered an oligomer, oligonucleotide, or polynucleotide. The nucleic acid can be DNA, RNA, or any nucleic acid analog, such as PNA, may be of genomic or synthetic origin, may be either double-stranded or single-stranded, and can represent either the sense or antisense (complementary) strand.

“Oligomer” refers to a nucleic acid sequence of at least about 6 nucleotides and as many as about 60 nucleotides, preferably about 15 to 40 nucleotides, and most preferably between about 20 and 30 nucleotides, that may be used in hybridization or amplification technologies. Oligomers may be used as, e.g., primers for PCR, and are usually chemically synthesized.

“Operably linked” refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

“Peptide nucleic acid” (PNA) refers to a DNA mimic in which nucleotide bases are attached to a pseudopeptide backbone to increase stability. PNAs, also designated antigene agents, can prevent gene expression by targeting complementary messenger RNA.

The phrases “percent identity” and “% identity”, as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and “diagonals saved”=4. The “weighted” residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the “percent similarity” between aligned polynucleotide sequence pairs.



Alternatively, a suite of commonly used and freely available sequence comparison algorithms can be used that are provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "BLASTN," that is used to determine alignment between a known polynucleotide sequence and other sequences on a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2/>. The "BLAST 2 Sequences" tool can be used for both BLASTN and BLASTP (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

*Matrix: BLOSUM62*  
*Reward for match: 1*  
*Penalty for mismatch: -2*  
*Open Gap: 5 and Extension Gap: 2 penalties*  
*Gap x drop-off: 50*  
*Expect: 10*  
*Word Size: 11*  
*Filter: on*

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity", as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a

standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the hydrophobicity and acidity of the substituted residue, thus preserving the structure (and therefore function) of the folded polypeptide.

5       Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default  
10       residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

          Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) with BLASTP set at default parameters. Such default parameters may be, for  
15       example:

*Matrix: BLOSUM62*  
          *Open Gap: 11 and Extension Gap: 1 penalty*  
          *Gap x drop-off: 50*  
          *Expect: 10*  
20       *Word Size: 3*  
          *Filter: on*

          Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for  
25       instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

          "Post-translational modification" of an MDDT may involve lipidation, glycosylation,  
30       phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu and the MDDT.

          "Probe" refers to mddt or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a  
35       detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands,

chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the figures and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al., (1989, Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY); Ausubel, F.M. et al., (1999, Short Protocols in Molecular Biology, 4<sup>th</sup> ed. Greene Publ. John Wiley & Sons Assoc. & Wiley-Intersciences, New York NY); and Innis, M. et al., (1990; PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA). PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved

regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

"Purified" refers to molecules, either polynucleotides or polypeptides that are isolated or separated from their natural environment and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other compounds with which they are naturally associated.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

"Regulatory element" refers to a nucleic acid sequence from nontranslated regions of a gene, and includes enhancers, promoters, introns, and 3' untranslated regions, which interact with host proteins to carry out or regulate transcription or translation.

"Reporter" molecules are chemical or biochemical moieties used for labeling a nucleic acid, an amino acid, or an antibody. They include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

"Sample" is used in its broadest sense. Samples may contain nucleic or amino acids, antibodies, or other materials, and may be derived from any source (e.g., bodily fluids including, but not limited to, saliva, blood, and urine; chromosome(s), organelles, or membranes isolated from a

cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; and cleared cells or tissues or blots or imprints from such cells or tissues).

“Specific binding” or “specifically binding” refers to the interaction between a protein or peptide and its agonist, antibody, antagonist, or other binding partner. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope “A,” the presence of a polypeptide containing epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

“Substitution” refers to the replacement of at least one nucleotide or amino acid by a different nucleotide or amino acid.

“Substrate” refers to any suitable rigid or semi-rigid support including, e.g., membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles or capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A “transcript image” or “expression profile” refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

“Transformation” refers to a process by which exogenous DNA enters a recipient cell. Transformation may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed.

“Transformants” include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as cells which transiently express inserted DNA or RNA.

A “transgenic organism,” as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, and plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection,

transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having  
5 at least 25% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 30%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater  
10 sequence identity over a certain defined length. The variant may result in "conservative" amino acid changes which do not affect structural and/or chemical properties. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The  
15 corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may  
20 encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

In an alternative, variants of the polynucleotides of the present invention may be generated through recombinant methods. One possible method is a DNA shuffling technique such as  
25 MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of MDDT, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene  
30 variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random  
35 point mutations may be recombined, screened, and then reshuffled until the desired properties are

optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

5 A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using BLASTP with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least  
10 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

## THE INVENTION

In a particular embodiment, cDNA sequences derived from human tissues and cell lines were  
15 aligned based on nucleotide sequence identity and assembled into "consensus" or "template" sequences which are designated by the template identification numbers (template IDs) in column 2 of Table 2. The sequence identification numbers (SEQ ID NO:s) corresponding to the template IDs are shown in column 1. The template sequences have similarity to GenBank sequences, or "hits," as designated by the GI Numbers in column 3. The statistical probability of each GenBank hit is  
20 indicated by a probability score in column 4, and the functional annotation corresponding to each GenBank hit is listed in column 5.

The invention incorporates the nucleic acid sequences of these templates as disclosed in the Sequence Listing and the use of these sequences in the diagnosis and treatment of disease states characterized by defects in disease detection and treatment molecules. The invention further utilizes  
25 these sequences in hybridization and amplification technologies, and in particular, in technologies which assess gene expression patterns correlated with specific cells or tissues and their responses in vivo or in vitro to pharmaceutical agents, toxins, and other treatments. In this manner, the sequences of the present invention are used to develop a transcript image for a particular cell or tissue.

### 30 Derivation of Nucleic Acid Sequences

cDNA was isolated from libraries constructed using RNA derived from normal and diseased human tissues and cell lines. The human tissues and cell lines used for cDNA library construction were selected from a broad range of sources to provide a diverse population of cDNAs representative of gene transcription throughout the human body. Descriptions of the human tissues and cell lines  
35 used for cDNA library construction are provided in the LIFESEQ database (Incyte Genomics, Inc.

(Incyte), Palo Alto CA). Human tissues were broadly selected from, for example, cardiovascular, dermatologic, endocrine, gastrointestinal, hematopoietic/immune system, musculoskeletal, neural, reproductive, and urologic sources.

Cell lines used for cDNA library construction were derived from, for example, leukemic  
5 cells, teratocarcinomas, neuroepitheliomas, cervical carcinoma, lung fibroblasts, and endothelial cells. Such cell lines include, for example, THP-1, Jurkat, HUVEC, hNT2, WI38, HeLa, and other cell lines commonly used and available from public depositories (American Type Culture Collection, Manassas VA). Prior to mRNA isolation, cell lines were untreated, treated with a pharmaceutical agent such as 5'-aza-2'-deoxycytidine, treated with an activating agent such as lipopolysaccharide in  
10 the case of leukocytic cell lines, or, in the case of endothelial cell lines, subjected to shear stress.

#### Sequencing of the cDNAs

Methods for DNA sequencing are well known in the art. Conventional enzymatic methods employ the Klenow fragment of DNA polymerase I, SEQUENASE DNA polymerase (U.S.  
15 Biochemical Corporation, Cleveland OH), Taq polymerase (Applied Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Inc. (Amersham Pharmacia Biotech), Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies Inc. (Life Technologies), Gaithersburg MD), to extend the nucleic acid sequence from an oligonucleotide primer annealed to the DNA  
20 template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. Chain termination reaction products may be electrophoresed on urea-polyacrylamide gels and detected either by autoradiography (for radioisotope-labeled nucleotides) or by fluorescence (for fluorophore-labeled nucleotides). Automated methods for mechanized reaction preparation, sequencing, and analysis using fluorescence detection methods have been developed.  
25 Machines used to prepare cDNAs for sequencing can include the MICROLAB 2200 liquid transfer system (Hamilton Company (Hamilton), Reno NV), Peltier thermal cycler (PTC200; MJ Research, Inc. (MJ Research), Watertown MA), and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing can be carried out using, for example, the ABI 373 or 377 (Applied Biosystems) or MEGABACE 1000 (Molecular Dynamics, Inc. (Molecular Dynamics), Sunnyvale  
30 CA) DNA sequencing systems, or other automated and manual sequencing systems well known in the art.

The nucleotide sequences of the Sequence Listing have been prepared by current, state-of-the-art, automated methods and, as such, may contain occasional sequencing errors or unidentified nucleotides. Such unidentified nucleotides are designated by an N. These infrequent unidentified  
35 bases do not represent a hindrance to practicing the invention for those skilled in the art. Several



methods employing standard recombinant techniques may be used to correct errors and complete the missing sequence information. (See, e.g., those described in Ausubel, F.M. et al. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY; and Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY.)

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#### Assembly of cDNA Sequences

Human polynucleotide sequences may be assembled using programs or algorithms well known in the art. Sequences to be assembled are related, wholly or in part, and may be derived from a single or many different transcripts. Assembly of the sequences can be performed using such  
10 programs as PHRAP (Phils Revised Assembly Program) and the GELVIEW fragment assembly system (GCG), or other methods known in the art.

Alternatively, cDNA sequences are used as "component" sequences that are assembled into "template" or "consensus" sequences as follows. Sequence chromatograms are processed, verified, and quality scores are obtained using PHRED. Raw sequences are edited using an editing pathway  
15 known as Block 1 (See, e.g., the LIFESEQ Assembled User Guide, Incyte Genomics, Palo Alto, CA). A series of BLAST comparisons is performed and low-information segments and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) are replaced by "n's", or masked, to prevent spurious matches. Mitochondrial and ribosomal RNA sequences are also removed. The processed sequences are then loaded into a relational database management system (RDMS) which assigns edited  
20 sequences to existing templates, if available. When additional sequences are added into the RDMS, a process is initiated which modifies existing templates or creates new templates from works in progress (i.e., nonfinal assembled sequences) containing queued sequences or the sequences themselves. After the new sequences have been assigned to templates, the templates can be merged into bins. If multiple templates exist in one bin, the bin can be split and the templates reannotated.

25 Once gene bins have been generated based upon sequence alignments, bins are "clone joined" based upon clone information. Clone joining occurs when the 5' sequence of one clone is present in one bin and the 3' sequence from the same clone is present in a different bin, indicating that the two bins should be merged into a single bin. Only bins which share at least two different clones are merged.

30 A resultant template sequence may contain either a partial or a full length open reading frame, or all or part of a genetic regulatory element. This variation is due in part to the fact that the full length cDNAs of many genes are several hundred, and sometimes several thousand, bases in length. With current technology, cDNAs comprising the coding regions of large genes cannot be cloned because of vector limitations, incomplete reverse transcription of the mRNA, or incomplete  
35 "second strand" synthesis. Template sequences may be extended to include additional contiguous

sequences derived from the parent RNA transcript using a variety of methods known to those of skill in the art. Extension may thus be used to achieve the full length coding sequence of a gene.

#### Analysis of the cDNA Sequences

5           The cDNA sequences are analyzed using a variety of programs and algorithms which are well known in the art. (See, e.g., Ausubel, 1997, supra, Chapter 7.7; Meyers, R.A. (Ed.) (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853; and Table 8.) These analyses comprise both reading frame determinations, e.g., based on triplet codon periodicity for particular organisms (Fickett, J.W. (1982) *Nucleic Acids Res.* 10:5303-5318); analyses of potential start and  
10 stop codons; and homology searches.

Computer programs known to those of skill in the art for performing computer-assisted searches for amino acid and nucleic acid sequence similarity, include, for example, Basic Local Alignment Search Tool (BLAST; Altschul, S.F. (1993) *J. Mol. Evol.* 36:290-300; Altschul, S.F. et al. (1990) *J. Mol. Biol.* 215:403-410). BLAST is especially useful in determining exact matches and  
15 comparing two sequence fragments of arbitrary but equal lengths, whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user (Karlin, S. et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:841-845). Using an appropriate search tool (e.g., BLAST or HMM), GenBank, SwissProt, BLOCKS, PFAM and other databases may be searched for sequences containing regions of homology to a query mddt or MDDT of the present  
20 invention.

Other approaches to the identification, assembly, storage, and display of nucleotide and polypeptide sequences are provided in "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S. Patent Number 5,953,727; and "Relational Database and System for Storing  
25 Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein in their entirety.

Protein hierarchies can be assigned to the putative encoded polypeptide based on, e.g., motif, BLAST, or biological analysis. Methods for assigning these hierarchies are described, for example, in "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence  
30 Data," U.S. Patent Number 6,023,659, incorporated herein by reference.

#### Human Disease Detection and Treatment Molecule Sequences

The mddt of the present invention may be used for a variety of diagnostic and therapeutic purposes. For example, an mddt may be used to diagnose a particular condition, disease, or disorder  
35 associated with disease detection and treatment molecules. Such conditions, diseases, and disorders

include, but are not limited to, a cell proliferative disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; and an autoimmune/inflammatory disorder, such as actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma. The mddt can be used to detect the presence of, or to quantify the amount of, an mddt-related polynucleotide in a sample. This information is then compared to information obtained from appropriate reference samples, and a diagnosis is established. Alternatively, a polynucleotide complementary to a given mddt can inhibit or inactivate a therapeutically relevant gene related to the mddt.

#### Analysis of mddt Expression Patterns

The expression of mddt may be routinely assessed by hybridization-based methods to determine, for example, the tissue-specificity, disease-specificity, or developmental stage-specificity of mddt expression. For example, the level of expression of mddt may be compared among different cell types or tissues, among diseased and normal cell types or tissues, among cell types or tissues at different developmental stages, or among cell types or tissues undergoing various treatments. This type of analysis is useful, for example, to assess the relative levels of mddt expression in fully or partially differentiated cells or tissues, to determine if changes in mddt expression levels are

correlated with the development or progression of specific disease states, and to assess the response of a cell or tissue to a specific therapy, for example, in pharmacological or toxicological studies.

Methods for the analysis of mddt expression are based on hybridization and amplification technologies and include membrane-based procedures such as northern blot analysis, high-throughput procedures that utilize, for example, microarrays, and PCR-based procedures.

#### Hybridization and Genetic Analysis

The mddt, their fragments, or complementary sequences, may be used to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid sequences. The mddt may be hybridized to naturally occurring or recombinant nucleic acid sequences under appropriately selected temperatures and salt concentrations. Hybridization with a probe based on the nucleic acid sequence of at least one of the mddt allows for the detection of nucleic acid sequences, including genomic sequences, which are identical or related to the mddt of the Sequence Listing. Probes may be selected from non-conserved or unique regions of at least one of the polynucleotides of SEQ ID NO:1-104 and tested for their ability to identify or amplify the target nucleic acid sequence using standard protocols.

Polynucleotide sequences that are capable of hybridizing, in particular, to those shown in SEQ ID NO:1-104 and fragments thereof, can be identified using various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions are discussed in "Definitions."

A probe for use in Southern or northern hybridization may be derived from a fragment of an mddt sequence, or its complement, that is up to several hundred nucleotides in length and is either single-stranded or double-stranded. Such probes may be hybridized in solution to biological materials such as plasmids, bacterial, yeast, or human artificial chromosomes, cleared or sectioned tissues, or to artificial substrates containing mddt. Microarrays are particularly suitable for identifying the presence of and detecting the level of expression for multiple genes of interest by examining gene expression correlated with, e.g., various stages of development, treatment with a drug or compound, or disease progression. An array analogous to a dot or slot blot may be used to arrange and link polynucleotides to the surface of a substrate using one or more of the following: mechanical (vacuum), chemical, thermal, or UV bonding procedures. Such an array may contain any number of mddt and may be produced by hand or by using available devices, materials, and machines.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) *Proc. Natl. Acad. Sci. USA* 94:2150-

2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

Probes may be labeled by either PCR or enzymatic techniques using a variety of commercially available reporter molecules. For example, commercial kits are available for radioactive and chemiluminescent labeling (Amersham Pharmacia Biotech) and for alkaline phosphatase labeling (Life Technologies). Alternatively, mddt may be cloned into commercially available vectors for the production of RNA probes. Such probes may be transcribed in the presence of at least one labeled nucleotide (e.g.,  $^{32}\text{P}$ -ATP, Amersham Pharmacia Biotech).

Additionally the polynucleotides of SEQ ID NO:1-104 or suitable fragments thereof can be used to isolate full length cDNA sequences utilizing hybridization and/or amplification procedures well known in the art, e.g., cDNA library screening, PCR amplification, etc. The molecular cloning of such full length cDNA sequences may employ the method of cDNA library screening with probes using the hybridization, stringency, washing, and probing strategies described above and in Ausubel, *supra*, Chapters 3, 5, and 6. These procedures may also be employed with genomic libraries to isolate genomic sequences of mddt in order to analyze, e.g., regulatory elements.

#### Genetic Mapping

Gene identification and mapping are important in the investigation and treatment of almost all conditions, diseases, and disorders. Cancer, cardiovascular disease, Alzheimer's disease, arthritis, diabetes, and mental illnesses are of particular interest. Each of these conditions is more complex than the single gene defects of sickle cell anemia or cystic fibrosis, with select groups of genes being predictive of predisposition for a particular condition, disease, or disorder. For example, cardiovascular disease may result from malfunctioning receptor molecules that fail to clear cholesterol from the bloodstream, and diabetes may result when a particular individual's immune system is activated by an infection and attacks the insulin-producing cells of the pancreas. In some studies, Alzheimer's disease has been linked to a gene on chromosome 21; other studies predict a different gene and location. Mapping of disease genes is a complex and reiterative process and generally proceeds from genetic linkage analysis to physical mapping.

As a condition is noted among members of a family, a genetic linkage map traces parts of chromosomes that are inherited in the same pattern as the condition. Statistics link the inheritance of particular conditions to particular regions of chromosomes, as defined by RFLP or other markers. (See, for example, Lander, E. S. and Botstein, D. (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.) Occasionally, genetic markers and their locations are known from previous studies. More often, however, the markers are simply stretches of DNA that differ among individuals. Examples of genetic linkage maps can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site.

In another embodiment of the invention, mddt sequences may be used to generate hybridization probes useful in chromosomal mapping of naturally occurring genomic sequences. Either coding or noncoding sequences of mddt may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of an mddt coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Meyers, supra, pp. 965-968.) Correlation between the location of mddt on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The mddt sequences may also be used to detect polymorphisms that are genetically linked to the inheritance of a particular condition, disease, or disorder.

In situ hybridization of chromosomal preparations and genetic mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending existing genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of the corresponding human chromosome is not known. These new marker sequences can be mapped to human chromosomes and may provide valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once a disease or syndrome has been crudely correlated by genetic linkage with a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequences of the subject invention may also be used to detect differences in chromosomal architecture due to translocation, inversion, etc., among normal, carrier, or affected individuals.

Once a disease-associated gene is mapped to a chromosomal region, the gene must be cloned in order to identify mutations or other alterations (e.g., translocations or inversions) that may be correlated with disease. This process requires a physical map of the chromosomal region containing the disease-gene of interest along with associated markers. A physical map is necessary for determining the nucleotide sequence of and order of marker genes on a particular chromosomal region. Physical mapping techniques are well known in the art and require the generation of

overlapping sets of cloned DNA fragments from a particular organelle, chromosome, or genome. These clones are analyzed to reconstruct and catalog their order. Once the position of a marker is determined, the DNA from that region is obtained by consulting the catalog and selecting clones from that region. The gene of interest is located through positional cloning techniques using hybridization  
5 or similar methods.

#### Diagnostic Uses

The mddt of the present invention may be used to design probes useful in diagnostic assays. Such assays, well known to those skilled in the art, may be used to detect or confirm conditions, disorders, or diseases associated with abnormal levels of mddt expression. Labeled probes developed  
10 from mddt sequences are added to a sample under hybridizing conditions of desired stringency. In some instances, mddt, or fragments or oligonucleotides derived from mddt, may be used as primers in amplification steps prior to hybridization. The amount of hybridization complex formed is quantified and compared with standards for that cell or tissue. If mddt expression varies significantly from the  
15 standard, the assay indicates the presence of the condition, disorder, or disease. Qualitative or quantitative diagnostic methods may include northern, dot blot, or other membrane or dip-stick based technologies or multiple-sample format technologies such as PCR, enzyme-linked immunosorbent assay (ELISA)-like, pin, or chip-based assays.

The probes described above may also be used to monitor the progress of conditions, disorders, or diseases associated with abnormal levels of mddt expression, or to evaluate the efficacy  
20 of a particular therapeutic treatment. The candidate probe may be identified from the mddt that are specific to a given human tissue and have not been observed in GenBank or other genome databases. Such a probe may be used in animal studies, preclinical tests, clinical trials, or in monitoring the treatment of an individual patient. In a typical process, standard expression is established by methods  
25 well known in the art for use as a basis of comparison, samples from patients affected by the disorder or disease are combined with the probe to evaluate any deviation from the standard profile, and a therapeutic agent is administered and effects are monitored to generate a treatment profile. Efficacy is evaluated by determining whether the expression progresses toward or returns to the standard normal pattern. Treatment profiles may be generated over a period of several days or several months.  
30 Statistical methods well known to those skilled in the art may be used to determine the significance of such therapeutic agents.

The polynucleotides are also useful for identifying individuals from minute biological samples, for example, by matching the RFLP pattern of a sample's DNA to that of an individual's DNA. The polynucleotides of the present invention can also be used to determine the actual  
35 base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be

used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, an individual can be identified through a unique set of DNA sequences. Once a unique ID database is established for an individual, positive identification of that individual can be made from extremely small tissue samples.

5 In a particular aspect, oligonucleotide primers derived from the mddt of the invention may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from mddt are  
10 used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the  
15 amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequences of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses  
20 of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

DNA-based identification techniques are critical in forensic technology. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood,  
25 saliva, semen, etc., can be amplified using, e.g., PCR, to identify individuals. (See, e.g., Erlich, H. (1992) PCR Technology, Freeman and Co., New York, NY). Similarly, polynucleotides of the present invention can be used as polymorphic markers.

There is also a need for reagents capable of identifying the source of a particular tissue. Appropriate reagents can comprise, for example, DNA probes or primers prepared from the  
30 sequences of the present invention that are specific for particular tissues. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention can also be used as molecular weight markers on nucleic acid gels or Southern blots, as diagnostic probes for the presence of a specific mRNA in a  
35 particular cell type, in the creation of subtracted cDNA libraries which aid in the discovery of novel



polynucleotides, in selection and synthesis of oligomers for attachment to an array or other support, and as an antigen to elicit an immune response.

#### Disease Model Systems Using mddt

The mddt of the invention or their mammalian homologs may be “knocked out” in an animal  
5 model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene,  
10 e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330).  
15 Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

The mddt of the invention may also be manipulated in vitro in ES cells derived from human  
20 blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

The mddt of the invention can also be used to create “knockin” humanized animals (pigs) or  
25 transgenic animals (mice or rats) to model human disease. With knockin technology, a region of mddt is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to  
30 overexpress mddt, resulting, e.g., in the secretion of MDDT in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

#### Screening Assays

MDDT encoded by polynucleotides of the present invention may be used to screen for  
35 molecules that bind to or are bound by the encoded polypeptides. The binding of the polypeptide and

the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the bound molecule. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a ligand or fragment thereof, a natural substrate, or a structural or functional mimetic. (See, Coligan et al., (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or to at least a fragment of the receptor, e.g., the active site. In either case, the molecule can be rationally designed using known techniques. Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing the polypeptide or cell membrane fractions which contain the expressed polypeptide are then contacted with a test compound and binding, stimulation, or inhibition of activity of either the polypeptide or the molecule is analyzed.

An assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. Alternatively, the assay may assess binding in the presence of a labeled competitor.

Additionally, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay using, e.g., a monoclonal or polyclonal antibody, can measure polypeptide level in a sample. The antibody can measure polypeptide level by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of the above assays can be used in a diagnostic or prognostic context. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

#### Transcript Imaging and Toxicological Testing

Another embodiment relates to the use of mddt to develop a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al.,

“Comparative Gene Transcript Analysis,” U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity pertaining to disease detection and treatment molecules.

Transcript images which profile mddt expression may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect mddt expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile mddt expression may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E. F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and Anderson, N. L. (2000) Toxicol. Lett. 112-113:467-71, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with

levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of MDDT encoded by polynucleotides of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for MDDT to quantify the levels of MDDT expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) Anal. Biochem. 270:103-11; Mendoze, L. G. et al. (1999) Biotechniques 27:778-88). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N. L. and Seilhamer, J. (1997) Electrophoresis 18:533-537), so proteome toxicant signatures may be

useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

5           In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic  
10       response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the MDDT encoded by polynucleotides of the present invention.

          In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are  
15       incubated with antibodies specific to the MDDT encoded by polynucleotides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

20       Transcript images may be used to profile mddt expression in distinct tissue types. This process can be used to determine disease detection and treatment molecule activity in a particular tissue type relative to this activity in a different tissue type. Transcript images may be used to generate a profile of mddt expression characteristic of diseased tissue. Transcript images of tissues before and after treatment may be used for diagnostic purposes, to monitor the progression of disease,  
25       and to monitor the efficacy of drug treatments for diseases which affect the activity of disease detection and treatment molecules.

          Transcript images of cell lines can be used to assess disease detection and treatment molecule activity and/or to identify cell lines that lack or misregulate this activity. Such cell lines may then be treated with pharmaceutical agents, and a transcript image following treatment may indicate the  
30       efficacy of these agents in restoring desired levels of this activity. A similar approach may be used to assess the toxicity of pharmaceutical agents as reflected by undesirable changes in disease detection and treatment molecule activity. Candidate pharmaceutical agents may be evaluated by comparing their associated transcript images with those of pharmaceutical agents of known effectiveness.

35       Antisense Molecules

The polynucleotides of the present invention are useful in antisense technology. Antisense technology or therapy relies on the modulation of expression of a target protein through the specific binding of an antisense sequence to a target sequence encoding the target protein or directing its expression. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa  
5 NJ; Alama, A. et al. (1997) *Pharmacol. Res.* 36(3):171-178; Crooke, S.T. (1997) *Adv. Pharmacol.* 40:1-49; Sharma, H.W. and R. Narayanan (1995) *Bioessays* 17(12):1055-1063; and Lavrosky, Y. et al. (1997) *Biochem. Mol. Med.* 62(1):11-22.) An antisense sequence is a polynucleotide sequence capable of specifically hybridizing to at least a portion of the target sequence. Antisense sequences bind to cellular mRNA and/or genomic DNA, affecting translation and/or transcription. Antisense  
10 sequences can be DNA, RNA, or nucleic acid mimics and analogs. (See, e.g., Rossi, J.J. et al. (1991) *Antisense Res. Dev.* 1(3):285-288; Lee, R. et al. (1998) *Biochemistry* 37(3):900-1010; Pardridge, W.M. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92(12):5592-5596; and Nielsen, P. E. and Haaima, G. (1997) *Chem. Soc. Rev.* 96:73-78.) Typically, the binding which results in modulation of expression occurs through hybridization or binding of complementary base pairs. Antisense sequences can also  
15 bind to DNA duplexes through specific interactions in the major groove of the double helix.

The polynucleotides of the present invention and fragments thereof can be used as antisense sequences to modify the expression of the polypeptide encoded by mddt. The antisense sequences can be produced ex vivo, such as by using any of the ABI nucleic acid synthesizer series (Applied Biosystems) or other automated systems known in the art. Antisense sequences can also be produced  
20 biologically, such as by transforming an appropriate host cell with an expression vector containing the sequence of interest. (See, e.g., Agrawal, supra.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence  
25 complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E., et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J., et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons,  
30 New York NY; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)

### Expression

In order to express a biologically active MDDT, the nucleotide sequences encoding MDDT or fragments thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding MDDT and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, supra, Chapters 4, 8, 16, and 17; and Ausubel, supra, Chapters 9, 10, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding MDDT. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal (mammalian) cell systems. (See, e.g., Sambrook, supra; Ausubel, 1995, supra, Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; Scorer, C.A. et al. (1994) Bio/Technology 12:181-184; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al., (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.)

The invention is not limited by the host cell employed.

For long term production of recombinant proteins in mammalian systems, stable expression of MDDT in cell lines is preferred. For example, sequences encoding MDDT can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector.

Any number of selection systems may be used to recover transformed cell lines. (See, e.g., Wigler,

M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.; Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14; Hartman, S.C. and R.C.Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051; Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

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#### Therapeutic Uses of mddt

The mddt of the invention may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and Somia, N. (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in mddt expression or regulation causes disease, the expression of mddt from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in mddt are treated by constructing mammalian expression vectors comprising mddt and introducing these vectors by mechanical means into mddt-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and Anderson, W.F. (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and Récipon, H. (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of mddt include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF,



PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). The mddt of the invention may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or  $\beta$ -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and Bujard, H. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:5547-5551; Gossen, M. et al., (1995) Science 268:1766-1769; Rossi, F.M.V. and Blau, H.M. (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding MDDT from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and Eb, A.J. (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al. (1982) EMBO J. 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to mddt expression are treated by constructing a retrovirus vector consisting of (i) mddt under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. U.S.A. 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and Miller, A.D. (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4<sup>+</sup> T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267;

Bonyhadi, M.L. (1997) *J. Virol.* 71:4707-4716; Ranga, U. et al. (1998) *Proc. Natl. Acad. Sci. U.S.A.* 95:1201-1206; Su, L. (1997) *Blood* 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver mddt to cells which have one or more genetic abnormalities with respect to the expression of mddt. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) *Transplantation* 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) *Annu. Rev. Nutr.* 19:511-544 and Verma, I.M. and Somia, N. (1997) *Nature* 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver mddt to target cells which have one or more genetic abnormalities with respect to the expression of mddt. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing mddt to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) *Exp. Eye Res.* 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W. F. et al. 1999 *J. Virol.* 73:519-532 and Xu, H. et al., (1994) *Dev. Biol.* 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver mddt to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and Li, K-J. (1998) *Curr. Opin. Biotech.* 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of

capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting mddt into the alphavirus genome in place of the capsid-coding region results in the production of a large number of mddt RNAs and the synthesis of high levels of MDDT in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of mddt into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

### Antibodies

Anti-MDDT antibodies may be used to analyze protein expression levels. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, and Fab fragments. For descriptions of and protocols of antibody technologies, see, e.g., Pound J.D. (1998)

Immunochemical Protocols, Humana Press, Totowa, NJ.

The amino acid sequence encoded by the mddt of the Sequence Listing may be analyzed by appropriate software (e.g., LASERGENE NAVIGATOR software, DNASTAR) to determine regions of high immunogenicity. The optimal sequences for immunization are selected from the C-terminus, the N-terminus, and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the polypeptide is in its natural conformation. Analysis used to select appropriate epitopes is also described by Ausubel (1997, supra, Chapter 11.7).

Peptides used for antibody induction do not need to have biological activity; however, they must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids, and most preferably at least 15 amino acids. A peptide which mimics an antigenic fragment of the natural polypeptide may be fused with another protein such as keyhole hemolimpet cyanin (KLH; Sigma, St. Louis MO) for antibody production. A peptide encompassing an antigenic region may be expressed from an mddt, synthesized as described above, or purified from human cells.

Procedures well known in the art may be used for the production of antibodies. Various hosts including mice, goats, and rabbits, may be immunized by injection with a peptide. Depending on the host species, various adjuvants may be used to increase immunological response.

In one procedure, peptides about 15 residues in length may be synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (Ausubel, 1995, supra). Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for anti-peptide activity by binding the peptide to plastic, blocking with 1% bovine serum albumin (BSA), reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG. Antisera with anti-peptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, radioimmunoassay (RIA), and immunoblotting.

In another procedure, isolated and purified peptide may be used to immunize mice (about 100  $\mu$ g of peptide) or rabbits (about 1 mg of peptide). Subsequently, the peptide is radioiodinated and used to screen the immunized animals' B-lymphocytes for production of anti-peptide antibodies. Positive cells are then used to produce hybridomas using standard techniques. About 20 mg of peptide is sufficient for labeling and screening several thousand clones. Hybridomas of interest are detected by screening with radioiodinated peptide to identify those fusions producing peptide-specific monoclonal antibody. In a typical protocol, wells of a multi-well plate (FAST, Becton-Dickinson, Palo Alto, CA) are coated with affinity-purified, specific rabbit-anti-mouse (or suitable anti-species IgG) antibodies at 10 mg/ml. The coated wells are blocked with 1% BSA and washed and exposed to supernatants from hybridomas. After incubation, the wells are exposed to radiolabeled peptide at 1 mg/ml.

Clones producing antibodies bind a quantity of labeled peptide that is detectable above background. Such clones are expanded and subjected to 2 cycles of cloning. Cloned hybridomas are injected into pristane-treated mice to produce ascites, and monoclonal antibody is purified from the ascitic fluid by affinity chromatography on protein A (Amersham Pharmacia Biotech). Several procedures for the production of monoclonal antibodies, including in vitro production, are described in Pound (supra). Monoclonal antibodies with anti-peptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

Antibody fragments containing specific binding sites for an epitope may also be generated. For example, such fragments include, but are not limited to, the F(ab')<sub>2</sub> fragments produced by pepsin digestion of the antibody molecule, and the Fab fragments generated by reducing the disulfide bridges of the F(ab')<sub>2</sub> fragments. Alternatively, construction of Fab expression libraries in filamentous bacteriophage allows rapid and easy identification of monoclonal fragments with desired specificity (Pound, supra, Chaps. 45-47). Antibodies generated against polypeptide encoded by mddt can be used to purify and characterize full-length MDDT protein and its activity, binding partners, etc.

### Assays Using Antibodies

Anti-MDDT antibodies may be used in assays to quantify the amount of MDDT found in a particular human cell. Such assays include methods utilizing the antibody and a label to detect expression level under normal or disease conditions. The peptides and antibodies of the invention may be used with or without modification or labeled by joining them, either covalently or  
5 noncovalently, with a reporter molecule.

Protocols for detecting and measuring protein expression using either polyclonal or monoclonal antibodies are well known in the art. Examples include ELISA, RIA, and fluorescent activated cell sorting (FACS). Such immunoassays typically involve the formation of complexes between the MDDT and its specific antibody and the measurement of such complexes. These and  
10 other assays are described in Pound (supra).

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

15 The disclosures of all patents, applications and publications, mentioned above and below, including U.S. Ser. No. 60/349,946 and U.S. 60/349,413, are hereby expressly incorporated by reference.

## EXAMPLES

### 20 I. Construction of cDNA Libraries

RNA was purchased from CLONTECH Laboratories, Inc. (Palo Alto CA) or isolated from various tissues. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The  
25 resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In most cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega Corporation (Promega), Madison WI),  
30 OLIGOTEX latex particles (QIAGEN, Inc. (QIAGEN), Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Inc., Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP  
35 vector system (Stratagene Cloning Systems, Inc. (Stratagene), La Jolla CA) or SUPERScript

plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, Chapters 5.1 through 6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), PCR2-TOPOTA plasmid (Invitrogen), PCMV-ICIS plasmid (Stratagene), pIGEN (Incyte Genomics, Palo Alto CA), pRARE (Incyte Genomics), or pINCY (Incyte Genomics), or derivatives thereof. Recombinant plasmids were transformed into competent E. coli cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 $\alpha$ , DH10B, or ElectroMAX DH10B from Life Technologies.

## II. Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: the Magic or WIZARD Minipreps DNA purification system (Promega); the AGTC Miniprep purification kit (Edge BioSystems, Gaithersburg MD); and the QIAWELL 8, QIAWELL 8 Plus, and QIAWELL 8 Ultra plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit (QIAGEN). Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format. (Rao, V.B. (1994) Anal. Biochem. 216:1-14.) Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Inc. (Molecular Probes), Eugene OR) and a FLUOROSKAN II fluorescence scanner (LabSystems Oy, Helsinki, Finland).

## III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 thermal cycler (Applied Biosystems) or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific Corp., Sunnyvale CA) or the MICROLAB 2200 liquid transfer system (Hamilton). cDNA

sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, Chapter 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

#### IV. Assembly and Analysis of Sequences

Component sequences from chromatograms were subject to PHRED analysis and assigned a quality score. The sequences having at least a required quality score were subject to various pre-processing editing pathways to eliminate, e.g., low quality 3' ends, vector and linker sequences, polyA tails, Alu repeats, mitochondrial and ribosomal sequences, bacterial contamination sequences, and sequences smaller than 50 base pairs. In particular, low-information sequences and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) were replaced by "n's", or masked, to prevent spurious matches.

Processed sequences were then subject to assembly procedures in which the sequences were assigned to gene bins (bins). Each sequence could only belong to one bin. Sequences in each gene bin were assembled to produce consensus sequences (templates). Subsequent new sequences were added to existing bins using BLASTN (v.1.4 WashU) and CROSSMATCH. Candidate pairs were identified as all BLAST hits having a quality score greater than or equal to 150. Alignments of at least 82% local identity were accepted into the bin. The component sequences from each bin were assembled using a version of PHRAP. Bins with several overlapping component sequences were assembled using DEEP PHRAP. The orientation (sense or antisense) of each assembled template was determined based on the number and orientation of its component sequences. Template sequences as disclosed in the sequence listing correspond to sense strand sequences (the "forward" reading frames), to the best determination. The complementary (antisense) strands are inherently disclosed herein. The component sequences which were used to assemble each template consensus sequence are listed in Table 5, along with their positions along the template nucleotide sequences.

Bins were compared against each other and those having local similarity of at least 82% were combined and reassembled. Reassembled bins having templates of insufficient overlap (less than 95% local identity) were re-split. Assembled templates were also subject to analysis by STITCHER/EXON MAPPER algorithms which analyze the probabilities of the presence of splice

variants, alternatively spliced exons, splice junctions, differential expression of alternative spliced genes across tissue types or disease states, etc. These resulting bins were subject to several rounds of the above assembly procedures.

Once gene bins were generated based upon sequence alignments, bins were clone joined  
5 based upon clone information. If the 5' sequence of one clone was present in one bin and the 3' sequence from the same clone was present in a different bin, it was likely that the two bins actually belonged together in a single bin. The resulting combined bins underwent assembly procedures to regenerate the consensus sequences.

The final assembled templates were subsequently annotated using the following procedure.  
10 Template sequences were analyzed using BLASTN (v2.0, NCBI) versus gbpri (GenBank version 135). "Hits" were defined as an exact match having from 95% local identity over 200 base pairs through 100% local identity over 100 base pairs, or a homolog match having an E-value, i.e. a probability score, of  $\leq 1 \times 10^{-8}$ . The hits were subject to frameshift FASTx versus GENPEPT (GenBank version 135). (See Table 8). In this analysis, a homolog match was defined as having an  
15 E-value of  $\leq 1 \times 10^{-8}$ . The assembly method used above was described in "System and Methods for Analyzing Biomolecular Sequences," U.S.S.N. 09/276,534, filed March 25, 1999, and the LIFESEQ Gold user manual (Incyte) both incorporated by reference herein.

Following assembly, template sequences were subjected to motif, BLAST, and functional analyses, and categorized in protein hierarchies using methods described in, e.g., "Database System  
20 Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S. Patent Number 6,023,659; "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S. Patent Number 5,953,727; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are  
25 incorporated by reference herein.

The template sequences were further analyzed by translating each template in all three forward reading frames and searching each translation against the Pfam database of hidden Markov model-based protein families and domains using the HMMER software package (available to the public from Washington University School of Medicine, St. Louis MO). Regions of templates which,  
30 when translated, contain similarity to Pfam consensus sequences are reported in Table 3, along with descriptions of Pfam protein domains and families. Only those Pfam hits with an E-value of  $\leq 1 \times 10^{-3}$  are reported. (See also World Wide Web site <http://pfam.wustl.edu/> for detailed descriptions of Pfam protein domains and families.)

Additionally, the template sequences were translated in all three forward reading frames, and  
35 each translation was searched against hidden Markov models for signal peptides using the HMMER



software package. Construction of hidden Markov models and their usage in sequence analysis has been described. (See, for example, Eddy, S.R. (1996) *Curr. Opin. Str. Biol.* 6:361-365.) Only those signal peptide hits with a cutoff score of 11 bits or greater are reported. A cutoff score of 11 bits or greater corresponds to at least about 91-94% true-positives in signal peptide prediction. Template sequences were also translated in all three forward reading frames, and each translation was searched against TMHMMER, a program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation (Sonnhammer, E.L. et al. (1998) *Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol.*, Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.) Regions of templates which, when translated, contain similarity to signal peptide or transmembrane consensus sequences are reported in Table 4.

The results of HMMER analysis as reported in Tables 3 and 4 may support the results of BLAST analysis as reported in Table 2 or may suggest alternative or additional properties of template-encoded polypeptides not previously uncovered by BLAST or other analyses.

Template sequences are further analyzed using the bioinformatics tools listed in Table 8, or using sequence analysis software known in the art such as MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Template sequences may be further queried against public databases such as the GenBank rodent, mammalian, vertebrate, prokaryote, and eukaryote databases.

The template sequences were translated to derive the corresponding longest open reading frame as presented by the polypeptide sequences as reported in Table 7. Alternatively, a polypeptide of the invention may begin at any of the methionine residues within the full length translated polypeptide. Polypeptide sequences were subsequently analyzed by querying against the GenBank protein database (GENPEPT, (GenBank version 135)). Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (GENPEPT) database. Column 1 shows the polypeptide sequence identification number (SEQ ID NO:) for the polypeptide segments of the invention. Column 2 shows the reading frame used in the translation of the polynucleotide sequences encoding the polypeptide segments. Column 3 shows the length of the translated polypeptide segments. Columns 4 and 5 show the start and stop nucleotide positions of the polynucleotide

sequences encoding the polypeptide segments. Column 6 shows the GenBank identification number (GI Number) of the nearest GenBank homolog. Column 7 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 8 shows the annotation of the GenBank homolog.

## 5 V. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

10 Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

15

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the  
 20 length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by  
 25 gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the  
 30 other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

## VI. Tissue Distribution Profiling

A tissue distribution profile is determined for each template by compiling the cDNA library  
 35 tissue classifications of its component cDNA sequences. Each component sequence, is derived from

a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. Template sequences, component sequences, and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

Table 6 shows the tissue distribution profile for the templates of the invention. For each template, the three most frequently observed tissue categories are shown in column 3, along with the percentage of component sequences belonging to each category. Only tissue categories with percentage values of  $\geq 10\%$  are shown. A tissue distribution of "widely distributed" in column 3 indicates percentage values of  $< 10\%$  in all tissue categories.

## VII. Transcript Image Analysis

Transcript images are generated as described in Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, incorporated herein by reference.

## VIII. Extension of Polynucleotide Sequences and Isolation of a Full-length cDNA

Oligonucleotide primers designed using an mddt of the Sequence Listing are used to extend the nucleic acid sequence. One primer is synthesized to initiate 5' extension of the template, and the other primer, to initiate 3' extension of the template. The initial primers may be designed using OLIGO 4.06 software (National Biosciences, Inc. (National Biosciences), Plymouth MN), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations are avoided. Selected human cDNA libraries are used to extend the sequence. If more than one extension is necessary or desired, additional or nested sets of primers are designed.

High fidelity amplification is obtained by PCR using methods well known in the art. PCR is performed in 96-well plates using the PTC-200 thermal cycler (MJ Research). The reaction mix contains DNA template, 200 nmol of each primer, reaction buffer containing  $Mg^{2+}$ ,  $(NH_4)_2SO_4$ , and  $\beta$ -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ are as follows: Step 1: 94°C, 3 min; Step 2:

94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well is determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v); Molecular Probes) dissolved in 1X Tris-EDTA (TE) and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Incorporated (Corning), Corning NY), allowing the DNA to bind to the reagent. The plate is scanned in a FLUOROSKAN II (Labsystems Oy) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 µl to 10 µl aliquot of the reaction mixture is analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions are successful in extending the sequence.

The extended nucleotides are desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides are separated on low concentration (0.6 to 0.8%) agarose gels, fragments are excised, and agar digested with AGAR ACE (Promega). Extended clones are religated using T4 ligase (New England Biolabs, Inc., Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells are selected on antibiotic-containing media, individual colonies are picked and cultured overnight at 37°C in 384-well plates in LB/2x carbenicillin liquid media.

The cells are lysed, and DNA is amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA is quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries are reamplified using the same conditions as described above. Samples are diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, the mddt is used to obtain regulatory sequences (promoters, introns, and enhancers) using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

## **IX. Labeling of Probes and Southern Hybridization Analyses**

Hybridization probes derived from the mddt of the Sequence Listing are employed for screening cDNAs, mRNAs, or genomic DNA. The labeling of probe nucleotides between 100 and

1000 nucleotides in length is specifically described, but essentially the same procedure may be used with larger cDNA fragments. Probe sequences are labeled at room temperature for 30 minutes using a T4 polynucleotide kinase,  $\gamma^{32}\text{P}$ -ATP, and 0.5X One-Phor-All Plus (Amersham Pharmacia Biotech) buffer and purified using a ProbeQuant G-50 Microcolumn (Amersham Pharmacia Biotech). The  
5 probe mixture is diluted to  $10^7$  dpm/ $\mu\text{g/ml}$  hybridization buffer and used in a typical membrane-based hybridization analysis.

The DNA is digested with a restriction endonuclease such as Eco RV and is electrophoresed through a 0.7% agarose gel. The DNA fragments are transferred from the agarose to nylon membrane (NYTRAN Plus, Schleicher & Schuell, Inc., Keene NH) using procedures specified by the  
10 manufacturer of the membrane. Prehybridization is carried out for three or more hours at  $68^\circ\text{C}$ , and hybridization is carried out overnight at  $68^\circ\text{C}$ . To remove non-specific signals, blots are sequentially washed at room temperature under increasingly stringent conditions, up to 0.1x saline sodium citrate (SSC) and 0.5% sodium dodecyl sulfate. After the blots are placed in a PHOSPHORIMAGER cassette (Molecular Dynamics) or are exposed to autoradiography film, hybridization patterns of  
15 standard and experimental lanes are compared. Essentially the same procedure is employed when screening RNA.

#### **X. Chromosome Mapping of mddt**

The cDNA sequences which were used to assemble SEQ ID NO:1-104 are compared with  
20 sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that match SEQ ID NO:1-104 are assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as PHRAP (Table 8). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for  
25 Genome Research (WIGR), and Généthon are used to determine if any of the clustered sequences have been previously mapped. Inclusion of a mapped sequence in a cluster will result in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location. The genetic map locations of SEQ ID NO:1-104 are described as ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus  
30 of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters.

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## XI. Microarray Analysis

### Probe Preparation from Tissue or Cell Samples

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and polyA<sup>+</sup> RNA is purified using the oligo (dT) cellulose method. Each polyA<sup>+</sup> RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ $\mu$ l oligo-dT primer (21mer), 1X first strand buffer, 0.03 units/ $\mu$ l RNase inhibitor, 500  $\mu$ M dATP, 500  $\mu$ M dGTP, 500  $\mu$ M dTTP, 40  $\mu$ M dCTP, 40  $\mu$ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng polyA<sup>+</sup> RNA with GEMBRIGHT kits (Incyte). Specific control polyA<sup>+</sup> RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA (W. Lei, unpublished). As quantitative controls, the control mRNAs at 0.002 ng, 0.02 ng, 0.2 ng, and 2 ng are diluted into reverse transcription reaction at ratios of 1:100,000, 1:10,000, 1:1000, 1:100 (w/w) to sample mRNA respectively. The control mRNAs are diluted into reverse transcription reaction at ratios of 1:3, 3:1, 1:10, 10:1, 1:25, 25:1 (w/w) to sample mRNA differential expression patterns. After incubation at 37° C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85° C to the stop the reaction and degrade the RNA. Probes are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The probe is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14  $\mu$ l 5X SSC/0.2% SDS.

### Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5  $\mu$ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester, PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1  $\mu$ l of the array element DNA, at an average concentration of 100 ng/ $\mu$ l, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

5        Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford, MA) for 30 minutes at 60° C followed by washes in 0.2% SDS and distilled water as before.

#### 10        Hybridization

Hybridization reactions contain 9  $\mu$ l of probe mixture consisting of 0.2  $\mu$ g each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The probe mixture is heated to 65° C for 5 minutes and is aliquoted onto the microarray surface and covered with  
15    an 1.8 cm<sup>2</sup> coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140  $\mu$ l of 5x SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60° C. The arrays are washed for 10 min at 45° C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45° C in a second wash buffer (0.1X SSC), and dried.

#### 20        Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is  
25    focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially.  
30    Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source,  
35    although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the probe mix at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two probes from  
5 different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital  
10 (A/D) conversion board (Analog Devices, Inc., Norwood, MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping  
15 emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte  
20 Genomics). Array elements that exhibit at least about a two-fold change in expression, a signal-to-background ratio of at least about 2.5, and an element spot size of at least about 40%, are considered to be differentially expressed.).

## **XII. Complementary Nucleic Acids**

Sequences complementary to the mddt are used to detect, decrease, or inhibit expression of  
25 the naturally occurring nucleotide. The use of oligonucleotides comprising from about 15 to 30 base pairs is typical in the art. However, smaller or larger sequence fragments can also be used. Appropriate oligonucleotides are designed from the mddt using OLIGO 4.06 software (National Biosciences) or other appropriate programs and are synthesized using methods standard in the art or  
30 ordered from a commercial supplier. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent transcription factor binding to the promoter sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding and processing of the transcript.

## **XIII. Expression of MDDT**

  
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Expression and purification of MDDT is accomplished using bacterial or virus-based expression systems. For expression of MDDT in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express MDDT upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of MDDT in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding MDDT by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See e.g., Engelhard, supra; and Sandig, supra.)

In most expression systems, MDDT is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from MDDT at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak Company, Rochester NY). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, Chapters 10 and 16). Purified MDDT obtained by these methods can be used directly in the following activity assay.

#### XIV. Demonstration of MDDT Activity

MDDT, or biologically active fragments thereof, are labeled with <sup>125</sup>I Bolton-Hunter reagent. (See, e.g., Bolton, A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled MDDT, washed, and any wells with labeled MDDT complex are assayed. Data obtained using different

concentrations of MDDT are used to calculate values for the number, affinity, and association of MDDT with the candidate molecules.

Alternatively, molecules interacting with MDDT are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (CLONTECH).

MDDT may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

#### 10 XV. Functional Assays

MDDT function is assessed by expressing mddt at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen Corporation, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10- $\mu$ g of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2  $\mu$ g of an additional plasmid containing sequences encoding a marker protein are co-transfected.

Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; CLONTECH), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties.

FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of MDDT on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding MDDT and either CD64 or CD64-GFP.

CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Inc., Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding MDDT and other genes of interest can be analyzed by northern analysis or microarray techniques.

#### **XVI. Production of Antibodies**

MDDT substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the MDDT amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding peptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, *supra*, Chapter 11.)

Typically, peptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, *supra*.) Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

#### **XVII. Purification of Naturally Occurring MDDT Using Specific Antibodies**

Naturally occurring or recombinant MDDT is substantially purified by immunoaffinity chromatography using antibodies specific for MDDT. An immunoaffinity column is constructed by covalently coupling anti-MDDT antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing MDDT are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of MDDT (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt

antibody/MDDT binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and MDDT is collected.

5 All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred  
10 embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
1	LG:1447398.9:2002JAN18	105	LG:1447398.9.orf2:2002JAN18
2	LG:201488.3:2002JAN18	106	LG:201488.3.orf3:2002JAN18
3	LG:288410.6:2002JAN18	107	LG:288410.6.orf2:2002JAN18
4	LG:7682817.1:2002JAN18	108	LG:7682817.1.orf3:2002JAN18
5	LG:7685059.6:2002JAN18	109	LG:7685059.6.orf2:2002JAN18
6	LG:7689671.1:2002JAN18	110	LG:7689671.1.orf2:2002JAN18
7	LG:7689684.1:2002JAN18	111	LG:7689684.1.orf2:2002JAN18
8	LG:7762669.1:2002JAN18	112	LG:7762669.1.orf1:2002JAN18
9	LG:965822.1:2002JAN18	113	LG:965822.1.orf1:2002JAN18
10	LG:006394.31:2002JAN18	114	LG:006394.31.orf2:2002JAN18
11	LG:018258.1:2002JAN18	115	LG:018258.1.orf2:2002JAN18
12	LG:027320.5:2002JAN18	116	LG:027320.5.orf3:2002JAN18
13	LG:057499.1:2002JAN18	117	LG:057499.1.orf1:2002JAN18
14	LG:065935.21:2002JAN18	118	LG:065935.21.orf2:2002JAN18
15	LG:071860.12:2002JAN18	119	LG:071860.12.orf3:2002JAN18
16	LG:087383.29:2002JAN18	120	LG:087383.29.orf2:2002JAN18
17	LG:098580.3:2002JAN18	121	LG:098580.3.orf2:2002JAN18
18	LG:1001879.1:2002JAN18	122	LG:1001879.1.orf1:2002JAN18
19	LG:1079456.4:2002JAN18	123	LG:1079456.4.orf3:2002JAN18
20	LG:1080598.9:2002JAN18	124	LG:1080598.9.orf2:2002JAN18
21	LG:1090358.10:2002JAN18	125	LG:1090358.10.orf1:2002JAN18
22	LG:1097492.2:2002JAN18	126	LG:1097492.2.orf2:2002JAN18
23	LG:1099945.26:2002JAN18	127	LG:1099945.26.orf2:2002JAN18
24	LG:110016.1:2002JAN18	128	LG:110016.1.orf1:2002JAN18
25	LG:1137613.10:2002JAN18	129	LG:1137613.10.orf2:2002JAN18
26	LG:118836.26:2002JAN18	130	LG:118836.26.orf2:2002JAN18
27	LG:1330261.32:2002JAN18	131	LG:1330261.32.orf1:2002JAN18
28	LG:1347461.28:2002JAN18	132	LG:1347461.28.orf3:2002JAN18
29	LG:1383494.16:2002JAN18	133	LG:1383494.16.orf3:2002JAN18
30	LG:1400155.1:2002JAN18	134	LG:1400155.1.orf2:2002JAN18
31	LG:1446621.1:2002JAN18	135	LG:1446621.1.orf3:2002JAN18
32	LG:144920.1:2002JAN18	136	LG:144920.1.orf1:2002JAN18
33	LG:1452619.1:2002JAN18	137	LG:1452619.1.orf2:2002JAN18
34	LG:1453417.6:2002JAN18	138	LG:1453417.6.orf1:2002JAN18
35	LG:148485.8:2002JAN18	139	LG:148485.8.orf1:2002JAN18
36	LG:1502670.1:2002JAN18	140	LG:1502670.1.orf2:2002JAN18
37	LG:206593.3:2002JAN18	141	LG:206593.3.orf2:2002JAN18
38	LG:228273.22:2002JAN18	142	LG:228273.22.orf1:2002JAN18
39	LG:228319.2:2002JAN18	143	LG:228319.2.orf1:2002JAN18
40	LG:229165.16:2002JAN18	144	LG:229165.16.orf2:2002JAN18
41	LG:230895.9:2002JAN18	145	LG:230895.9.orf1:2002JAN18
42	LG:233552.5:2002JAN18	146	LG:233552.5.orf1:2002JAN18
43	LG:234430.7:2002JAN18	147	LG:234430.7.orf3:2002JAN18
44	LG:236659.1:2002JAN18	148	LG:236659.1.orf3:2002JAN18
45	LG:236767.26:2002JAN18	149	LG:236767.26.orf2:2002JAN18
46	LG:237489.7:2002JAN18	150	LG:237489.7.orf1:2002JAN18
47	LG:238218.20:2002JAN18	151	LG:238218.20.orf1:2002JAN18
48	LG:239939.14:2002JAN18	152	LG:239939.14.orf3:2002JAN18
49	LG:242288.11:2002JAN18	153	LG:242288.11.orf1:2002JAN18
50	LG:242491.29:2002JAN18	154	LG:242491.29.orf1:2002JAN18

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
51	LG:243488.41:2002JAN18	155	LG:243488.41.orf3:2002JAN18
52	LG:247792.18:2002JAN18	156	LG:247792.18.orf2:2002JAN18
53	LG:253193.17:2002JAN18	157	LG:253193.17.orf3:2002JAN18
54	LG:257088.20:2002JAN18	158	LG:257088.20.orf2:2002JAN18
55	LG:265552.1:2002JAN18	159	LG:265552.1.orf2:2002JAN18
56	LG:275355.12:2002JAN18	160	LG:275355.12.orf1:2002JAN18
57	LG:280014.1:2002JAN18	161	LG:280014.1.orf1:2002JAN18
58	LG:299937.3:2002JAN18	162	LG:299937.3.orf3:2002JAN18
59	LG:311197.3:2002JAN18	163	LG:311197.3.orf3:2002JAN18
60	LG:321069.2:2002JAN18	164	LG:321069.2.orf1:2002JAN18
61	LG:330900.8:2002JAN18	165	LG:330900.8.orf2:2002JAN18
62	LG:330931.9:2002JAN18	166	LG:330931.9.orf1:2002JAN18
63	LG:330985.1:2002JAN18	167	LG:330985.1.orf3:2002JAN18
64	LG:332027.9:2002JAN18	168	LG:332027.9.orf3:2002JAN18
65	LG:335377.8:2002JAN18	169	LG:335377.8.orf2:2002JAN18
66	LG:337452.25:2002JAN18	170	LG:337452.25.orf3:2002JAN18
67	LG:340580.16:2002JAN18	171	LG:340580.16.orf2:2002JAN18
68	LG:350272.6:2002JAN18	172	LG:350272.6.orf2:2002JAN18
69	LG:397228.1:2002JAN18	173	LG:397228.1.orf1:2002JAN18
70	LG:401325.41:2002JAN18	174	LG:401325.41.orf2:2002JAN18
71	LG:402029.14:2002JAN18	175	LG:402029.14.orf3:2002JAN18
72	LG:407233.2:2002JAN18	176	LG:407233.2.orf3:2002JAN18
73	LG:407346.1:2002JAN18	177	LG:407346.1.orf3:2002JAN18
74	LG:407689.7:2002JAN18	178	LG:407689.7.orf3:2002JAN18
75	LG:407700.1:2002JAN18	179	LG:407700.1.orf2:2002JAN18
76	LG:410461.92:2002JAN18	180	LG:410461.92.orf3:2002JAN18
77	LG:411043.3:2002JAN18	181	LG:411043.3.orf2:2002JAN18
78	LG:438690.47:2002JAN18	182	LG:438690.47.orf1:2002JAN18
79	LG:444677.81:2002JAN18	183	LG:444677.81.orf1:2002JAN18
80	LG:457464.24:2002JAN18	184	LG:457464.24.orf3:2002JAN18
81	LG:7684793.15:2002JAN18	185	LG:7684793.15.orf3:2002JAN18
82	LG:7687485.1:2002JAN18	186	LG:7687485.1.orf1:2002JAN18
83	LG:7689661.4:2002JAN18	187	LG:7689661.4.orf2:2002JAN18
84	LG:7690373.1:2002JAN18	188	LG:7690373.1.orf1:2002JAN18
85	LG:7696560.1:2002JAN18	189	LG:7696560.1.orf3:2002JAN18
86	LG:7698190.26:2002JAN18	190	LG:7698190.26.orf3:2002JAN18
87	LG:7763560.12:2002JAN18	191	LG:7763560.12.orf1:2002JAN18
88	LG:7763587.20:2002JAN18	192	LG:7763587.20.orf2:2002JAN18
89	LG:899263.10:2002JAN18	193	LG:899263.10.orf2:2002JAN18
90	LG:977837.31:2002JAN18	194	LG:977837.31.orf1:2002JAN18
91	LG:978560.13:2002JAN18	195	LG:978560.13.orf2:2002JAN18
92	LG:979390.2:2002JAN18	196	LG:979390.2.orf1:2002JAN18
93	LG:983019.1:2002JAN18	197	LG:983019.1.orf2:2002JAN18
94	LG:997202.7:2002JAN18	198	LG:997202.7.orf2:2002JAN18
95	LG:998756.3:2002JAN18	199	LG:998756.3.orf1:2002JAN18
96	LG:103460.28:2002JAN18	200	LG:103460.28.orf2:2002JAN18
97	LG:1501505.19:2002JAN18	201	LG:1501505.19.orf1:2002JAN18
98	LG:233444.9:2002JAN18	202	LG:233444.9.orf2:2002JAN18
99	LG:234824.7:2002JAN18	203	LG:234824.7.orf2:2002JAN18
100	LG:235708.23:2002JAN18	204	LG:235708.23.orf1:2002JAN18

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
101	LG:236649.14:2002JAN18	205	LG:236649.14.orf1:2002JAN18
102	LG:332474.7:2002JAN18	206	LG:332474.7.orf1:2002JAN18
103	LG:335727.8:2002JAN18	207	LG:335727.8.orf2:2002JAN18
104	LG:481983.1:2002JAN18	208	LG:481983.1.orf3:2002JAN18

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
1	LG:1447398.9:2002JAN18	g21748992	0.00	Homo sapiens cDNA FLJ33450 fis, clone BRAMY2000025.
2	LG:201488.3:2002JAN18	g6599307	4.00E-98	LIM domains containing protein 1 (Mus musculus)
3	LG:288410.6:2002JAN18	g15823642	0.00	ALS2CR7 (Homo sapiens)
4	LG:7682817.1:2002JAN18	g18203798	1.00E-97	Homo sapiens, clone MGC:15956 IMAGE:3538227, mRNA, complete cds.
5	LG:7685059.6:2002JAN18	g21750806	0.00	Homo sapiens cDNA FLJ34942 fis, clone NT2RP7007530, moderately similar to ZINC FINGER PROTEIN 211.
6	LG:7689671.1:2002JAN18	g22477160	8.00E-45	Homo sapiens, clone IMAGE:4846514, mRNA, partial cds.
7	LG:7689684.1:2002JAN18	g21750781	0.00	Homo sapiens cDNA FLJ34921 fis, clone NT2RP7002978, moderately similar to ZINC FINGER PROTEIN ZFP-36.
8	LG:7762669.1:2002JAN18	g21754721	1.00E-85	Homo sapiens cDNA FLJ38144 fis, clone D9OST2003397, moderately similar to ZINC FINGER PROTEIN 91.
9	LG:965822.1:2002JAN18	g21955442	0.00	Homo sapiens, Similar to zinc finger protein 331; zinc finger protein 463, clone IMAGE:3920900, mRNA.
10	LG:006394.31:2002JAN18	g20987337	0.00	Homo sapiens, clone IMAGE:4748060, mRNA, partial cds.
11	LG:018258.1:2002JAN18	g19483967	1.00E-110	RIKEN cDNA O610009A07 gene (Mus musculus)
12	LG:027320.5:2002JAN18	g9967126	0.00	Macaca fascicularis brain cDNA, clone:QcccE-17586.
13	LG:057499.1:2002JAN18	g12407440	0.00	Homo sapiens tripartite motif protein TRIM33 alpha (TRIM33) mRNA, complete cds; alternatively spliced.
14	LG:065935.21:2002JAN18	g23273088	0.00	Homo sapiens, clone MGC:43081 IMAGE:5259721, mRNA, complete cds.
15	LG:071860.12:2002JAN18	g17390472	1.00E-123	Homo sapiens, mago-nashi (Drosophila) homolog, proliferation-associated, clone MGC:17367 IMAGE:3861094, mRNA, complete cds.
16	LG:087383.29:2002JAN18	g12053194	0.00	Homo sapiens mRNA; cDNA DKFZp434H1130 (from clone DKFZp434H1130); complete cds.
17	LG:098580.3:2002JAN18	g20069117	0.00	Homo sapiens caspase 12 variant alpha (CASP12) mRNA, complete sequence; alternatively spliced.
18	LG:1001879.1:2002JAN18	g21886479	0.00	unnamed protein product (Homo sapiens)
19	LG:1079456.4:2002JAN18	g22760915	0.00	Homo sapiens cDNA FLJ90585 fis, clone PLACE1000907, highly similar to ZINC FINGER PROTEIN 83.
20	LG:1080598.9:2002JAN18	g21618498	0.00	Homo sapiens, Similar to hypothetical protein FLJ20079, clone MGC:45408 IMAGE:5540009, mRNA, complete cds.



Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
21	LG:1090358.10:2002JAN18	g21749606	0.00	Homo sapiens cDNA FLJ33955 fis, clone CTONG2018652, moderately similar to ZINC FINGER PROTEIN MFG-3.
22	LG:1097492.2:2002JAN18	g10047329	0.00	KIAA1626 protein (Homo sapiens)
23	LG:1099945.26:2002JAN18	g6808024	0.00	Homo sapiens mRNA; cDNA DKFZp434J0428 (from clone DKFZp434J0428).
24	LG:110016.1:2002JAN18	g16552018	0.00	Homo sapiens cDNA FLJ32015 fis, clone NTONG1000052, weakly similar to Rattus norvegicus mRNA for Kelch related protein 1.
25	LG:1137613.10:2002JAN18	g14789616	1.00E-175	Homo sapiens, Similar to RIKEN cDNA 6720463E02 gene, clone MGC:17810 IMAGE:3891655, mRNA, complete cds.
26	LG:118836.26:2002JAN18	g12667437	0.00	Homo sapiens NIR3 mRNA, complete cds.
27	LG:1330261.32:2002JAN18	g22761032	0.00	unnamed protein product (Homo sapiens)
28	LG:1347461.28:2002JAN18	g21755436	0.00	Homo sapiens cDNA FLJ38725 fis, clone KIDNE2010265.
29	LG:1383494.16:2002JAN18	g16741479	0.00	Homo sapiens, CGI-100 protein, clone MGC:5366 IMAGE:3048959, mRNA, complete cds.
30	LG:1400155.1:2002JAN18	g556220	0.00	Human NAD+-dependent succinate-semialdehyde dehydrogenase (SSADH) mRNA, 3' end.
31	LG:1446621.1:2002JAN18	g16306805	1.00E-105	Homo sapiens, zinc finger protein 43 (HTF6), clone MGC:10581 IMAGE:3687640, mRNA, complete cds.
32	LG:144920.1:2002JAN18	g2689444	1.00E-141	ZNF134 (Homo sapiens)
33	LG:1452619.1:2002JAN18	g9246972	0.00	Homo sapiens RNA-binding protein BRUNOL2 (BRUNOL2) mRNA, complete cds.
34	LG:1453417.6:2002JAN18	g1665821	0.00	Similar to D.melanogaster cadherin-related tumor suppressor (Homo sapiens)
35	LG:148485.8:2002JAN18	g21595467	0.00	Homo sapiens, clone MGC:40579 IMAGE:5217372, mRNA, complete cds.
36	LG:1502670.1:2002JAN18	g21755190	0.00	Homo sapiens cDNA FLJ38528 fis, clone HCHON2000942.
37	LG:206593.3:2002JAN18	g16551839	0.00	Homo sapiens cDNA FLJ31875 fis, clone NT2RP7002450, weakly similar to ZINC FINGER PROTEIN 84.
38	LG:228273.22:2002JAN18	g3327175	0.00	Homo sapiens mRNA for KIAA0681 protein, partial cds.
39	LG:228319.2:2002JAN18	g21752073	0.00	unnamed protein product (Homo sapiens)
40	LG:229165.16:2002JAN18	g3970716	0.00	Homo sapiens mRNA for KET protein.
41	LG:230895.9:2002JAN18	g15620894	0.00	Homo sapiens mRNA for KIAA1918 protein, partial cds.
42	LG:233552.5:2002JAN18	g10047282	0.00	Homo sapiens mRNA for KIAA1604 protein, partial cds.

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Anotation
43	LG:234430.7:2002JAN18	g12653106	0.00	Homo sapiens, hypothetical protein dJ37E16.5, clone MGC:8472 IMAGE:2821743, mRNA, complete cds.
44	LG:236659.1:2002JAN18	g12083895	0.00	Homo sapiens polybromo-1 (PB1) mRNA, complete cds, alternatively spliced.
45	LG:236767.26:2002JAN18	g18916868	0.00	Homo sapiens mRNA for KIAA1978 protein.
46	LG:237489.7:2002JAN18	g16588680	0.00	Homo sapiens anion transporter/exchanger-9 (SLC26A9) mRNA, complete
47	LG:238218.20:2002JAN18	g19116222	0.00	Homo sapiens, clone MGC:9833 IMAGE:3863491, mRNA, complete cds.
48	LG:239939.14:2002JAN18	g21758739	0.00	Homo sapiens cDNA FLJ25797 fis, clone IST07046.
49	LG:242288.11:2002JAN18	g4164385	0.00	PAK4 protein (Homo sapiens)
50	LG:242491.29:2002JAN18	g22760074	0.00	Homo sapiens cDNA FLJ90076 fis, clone HEMBA1004444, moderately similar to GLYCOPROTEIN 25L PRECURSOR.
51	LG:243488.41:2002JAN18	g21542540	0.00	Homo sapiens, Similar to HTPAP protein, clone MGC:32924 IMAGE:5267610, mRNA, complete cds.
52	LG:247792.18:2002JAN18	g21739660	0.00	Homo sapiens mRNA: cDNA DKFZp434L1426 (from clone DKFZp434L1426).
53	LG:253193.17:2002JAN18	g20988139	0.00	Homo sapiens, E74-like factor 1 (ets domain transcription factor), clone MGC:40398 IMAGE:4385989, mRNA, complete cds.
54	LG:257088.20:2002JAN18	g20372683	0.00	euchromatic histone methyltransferase 1 (Homo sapiens)
55	LG:265552.1:2002JAN18	g18490501	1.00E-100	RIKEN cDNA 2010002A20 gene (Mus musculus)
56	LG:275355.12:2002JAN18	g17223623	0.00	Homo sapiens ATP-binding cassette A9 mRNA, complete cds.
57	LG:280014.1:2002JAN18	g18088579	0.00	Homo sapiens, clone MGC:23949 IMAGE:4243903, mRNA, complete cds.
58	LG:299937.3:2002JAN18	g10439753	0.00	Homo sapiens cDNA: FLJ23158 fis, clone LNG09623.
59	LG:311197.3:2002JAN18	g21750727	0.00	Homo sapiens cDNA FLJ34876 fis, clone NT2NE2015362, moderately similar to Mitogen inducible gene mlg-2.
60	LG:321069.2:2002JAN18	g18677068	0.00	Homo sapiens cDNA FLJ23877 fis, clone LNG13624.
61	LG:330900.8:2002JAN18	g18043698	0.00	PRO2000 protein (Homo sapiens)
62	LG:330931.9:2002JAN18	g16551908	0.00	Homo sapiens cDNA FLJ31930 fis, clone NT2RP7006162, weakly similar to ZINC FINGER PROTEIN MFG-3.
63	LG:330985.1:2002JAN18	g1222522	0.00	Human placental folate transporter (hFOLT1) mRNA, complete cds.
64	LG:332027.9:2002JAN18	g21749635	0.00	Homo sapiens cDNA FLJ33979 fis, clone DFNES2004371.
65	LG:335377.8:2002JAN18	g16550148	0.00	Homo sapiens cDNA FLJ30864 fis, clone FEBRA2004091, highly similar to Homo sapiens RING finger protein terf mRNA.

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
66	LG:337452.25:2002JAN18	g16549250	0.00	Homo sapiens cDNA FLJ30100 fis, clone BNGH41000104.
67	LG:340580.16:2002JAN18	g10434656	0.00	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321.
68	LG:350272.6:2002JAN18	g22859174	0.00	hypothetical protein (Homo sapiens)
69	LG:397228.1:2002JAN18	g15741221	1.00E-17	gene overexpressed in astrocytoma (Homo sapiens)
70	LG:401325.41:2002JAN18	g4126475	0.00	BAP2-alpha protein (Homo sapiens)
71	LG:402029.14:2002JAN18	g10437932	0.00	Homo sapiens cDNA: FLJ21771 fis, clone COLF7779.
72	LG:407233.2:2002JAN18	g20810035	0.00	Homo sapiens, Fc receptor-like protein 3, clone MGC:34866 IMAGE:4340939, mRNA, complete cds.
73	LG:407346.1:2002JAN18	g21753085	0.00	unnamed protein product (Homo sapiens)
74	LG:407689.7:2002JAN18	g13365844	0.00	Macaca fascicularis brain cDNA clone:QcccE-19502, full insert sequence.
75	LG:407700.1:2002JAN18	g14198271	0.00	Homo sapiens, clone MGC:5352 IMAGE:3048106, mRNA, complete cds.
76	LG:410461.92:2002JAN18	g16877725	0.00	Homo sapiens, likely ortholog of mouse g1-related zinc finger protein, clone MGC:15167 IMAGE:3535930, mRNA, complete cds.
77	LG:411043.3:2002JAN18	g21755898	0.00	unnamed protein product (Homo sapiens)
78	LG:438690.47:2002JAN18	g10434222	0.00	Homo sapiens cDNA FLJ12622 fis, clone NT2RM4001731, highly similar to Homo sapiens F-box protein Lillia (LILINA) mRNA.
79	LG:444677.81:2002JAN18	g4929678	0.00	Homo sapiens CGI-105 protein mRNA, complete cds.
80	LG:457464.24:2002JAN18	g12653266	0.00	Homo sapiens, fusion, derived from t(12;16) malignant liposarcoma, clone MGC:8537 IMAGE:2822692, mRNA, complete cds.
81	LG:7684793.15:2002JAN18	g12275895	0.00	tripartite motif protein TRIM19 gamma (Homo sapiens)
82	LG:7687485.1:2002JAN18	g21752508	0.00	Homo sapiens cDNA FLJ36280 fis, clone THYMU2003282, moderately similar to ZINC FINGER PROTEIN 135.
83	LG:7689661.4:2002JAN18	g21739829	0.00	Homo sapiens mRNA; cDNA DKFp761C148 (from clone DKFp761C148); complete cds.
84	LG:7690373.1:2002JAN18	g21757678	0.00	Homo sapiens cDNA FLJ40479 fis, clone TEST12043282, moderately similar to ZINC FINGER PROTEIN 43.
85	LG:7696560.1:2002JAN18	g21752388	0.00	Homo sapiens cDNA FLJ36178 fis, clone TEST12026534.
86	LG:7698190.26:2002JAN18	g4914583	0.00	Homo sapiens mRNA; cDNA DKFp586A032 (from clone DKFp586A032); partial cds.
87	LG:7763560.12:2002JAN18	g12005677	0.00	Homo sapiens HT029 mRNA, complete cds.

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
88	LG:7763587.20:2002JAN18	g12803700	0.00	Homo sapiens, ankyrin repeat-containing protein, clone MGC:3528 IMAGE:3607648, mRNA, complete cds.
89	LG:899263.10:2002JAN18	g21750988	0.00	Homo sapiens cDNA FLJ35084 fs, clone PLACE6005482.
90	LG:977837.31:2002JAN18	g22760683	0.00	Homo sapiens cDNA FLJ90440 fs, clone NT2RP3000921, weakly similar to TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
91	LG:978560.13:2002JAN18	g10047251	0.00	KIAA1588 protein (Homo sapiens)
92	LG:979390.2:2002JAN18	g21756044	1.00E-180	Homo sapiens cDNA FLJ39208 fs, clone OCBBF2006030.
93	LG:983019.1:2002JAN18	g23336960	0.00	Homo sapiens, Similar to eomesodermin homolog (Xenopus laevis), clone IMAGE:5223017, mRNA.
94	LG:997202.7:2002JAN18	g12803934	0.00	Homo sapiens, clone IMAGE:3638276, mRNA, partial cds.
95	LG:998756.3:2002JAN18	g24181969	0.00	NEW1 domain containing protein isoform (Homo sapiens)
96	LG:103460.28:2002JAN18	g7023281	0.00	Homo sapiens cDNA FLJ10927 fs, clone OVARC1000466.
97	LG:1501505.19:2002JAN18	g15929456	0.00	Homo sapiens, clone IMAGE:3885940, mRNA, partial cds.
98	LG:233444.9:2002JAN18	g7023136	0.00	unnamed protein product (Homo sapiens)
99	LG:234824.7:2002JAN18	g15879022	0.00	Homo sapiens genomic sequence surrounding NotI site, clone NL1-CP10R.
100	LG:235708.23:2002JAN18	g22760880	0.00	Homo sapiens cDNA FLJ90562 fs, clone OVARC1001163.
101	LG:236649.14:2002JAN18	g20067239	1.00E-118	putative regulation protein GS3 (Rattus norvegicus)
102	LG:332474.7:2002JAN18	g21755742	0.00	Homo sapiens cDNA FLJ38969 fs, clone NT2R12002359.
103	LG:335727.8:2002JAN18	g16554117	0.00	Homo sapiens cDNA FLJ25361 fs, clone TS101713.
104	LG:481983.1:2002JAN18	g21410797	0.00	Homo sapiens, clone IMAGE:4396549, mRNA, partial cds.

TABLE 3

SEQ ID NO.	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
1	LG:1447398.9:2002JAN18	677	754	forward 2	RPEL	RPEL repeat	7.40E-14
2	LG:201488.3:2002JAN18	57	233	forward 3	LIM	LIM domain	2.10E-29
3	LG:288410.6:2002JAN18	443	1099	forward 2	pknase	Protein kinase domain	7.40E-05
3	LG:288410.6:2002JAN18	243	1091	forward 3	pknase	Protein kinase domain	3.70E-09
4	LG:7682817.1:2002JAN18	898	1074	forward 1	Ribosomal_S5	Ribosomal protein S5, N-terminal domain	0.00051
5	LG:7685059.6:2002JAN18	314	436	forward 2	KRAB	KRAB box	1.90E-24
6	LG:7689671.1:2002JAN18	317	439	forward 2	KRAB	KRAB box	1.90E-26
7	LG:7689684.1:2002JAN18	188	310	forward 2	KRAB	KRAB box	8.20E-24
8	LG:7762669.1:2002JAN18	178	300	forward 1	KRAB	KRAB box	2.90E-26
9	LG:965822.1:2002JAN18	424	546	forward 1	KRAB	KRAB box	6.50E-25
10	LG:006394.31:2002JAN18	1790	2248	forward 2	RhoGAP	RhoGAP domain	6.10E-57
10	LG:006394.31:2002JAN18	228	317	forward 3	WW	WW domain	3.20E-05
11	LG:018258.1:2002JAN18	299	718	forward 2	Nitroreductase	Nitroreductase family	9.50E-05
12	LG:027320.5:2002JAN18	132	332	forward 3	SAM	SAM domain (Sterile alpha motif)	6.30E-06
13	LG:057499.1:2002JAN18	1306	1575	forward 1	bromodomain	Bromodomain	4.10E-18
13	LG:057499.1:2002JAN18	1087	1224	forward 1	PHD	PHD-finger	2.70E-12
14	LG:065935.21:2002JAN18	209	517	forward 2	HesB-like	HesB-like domain	3.50E-36
15	LG:071860.12:2002JAN18	426	773	forward 3	Mago_nashi	Mago nashi protein	2.40E-19
16	LG:087383.29:2002JAN18	173	439	forward 2	FCH	Fes/CIP4 homology domain	2.90E-30
17	LG:098580.3:2002JAN18	74	331	forward 2	ICE_p10	ICE-like protease (caspase) p10 domain	1.30E-31
18	LG:1001879.1:2002JAN18	310	381	forward 1	LRR	Leucine Rich Repeat	1.60E-40
18	LG:1001879.1:2002JAN18	217	306	forward 1	LRRNT	Leucine rich repeat N-terminal domain	4.40E-07
18	LG:1001879.1:2002JAN18	1204	1365	forward 1	LRRCT	Leucine rich repeat C-terminal domain	7.20E-05
19	LG:1079456.4:2002JAN18	398	520	forward 2	KRAB	KRAB box	1.00E-28
19	LG:1079456.4:2002JAN18	183	305	forward 3	KRAB	KRAB box	4.00E-24
20	LG:1080598.9:2002JAN18	755	823	forward 2	zf-C2H2	Zinc finger, C2H2 type	8.00E-59
20	LG:1080598.9:2002JAN18	524	646	forward 2	KRAB	KRAB box	1.80E-22
21	LG:1090358.10:2002JAN18	808	930	forward 1	KRAB	KRAB box	3.90E-27
21	LG:1090358.10:2002JAN18	1285	1353	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.20E-22
21	LG:1090358.10:2002JAN18	1452	1520	forward 3	zf-C2H2	Zinc finger, C2H2 type	5.80E-52
22	LG:1097492.2:2002JAN18	691	1194	forward 1	RhoGEF	RhoGEF domain	2.00E-05

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
23	LG:109945.26:2002JAN18	236	364	forward 2	Ribosomal_L37e	Ribosomal protein L37e	1.80E-06
24	LG:110016.1:2002JAN18	1337	1477	forward 2	Kelch	Kelch motif	1.30E-23
24	LG:110016.1:2002JAN18	135	452	forward 3	BTB	BTB/POZ domain	8.40E-35
25	LG:1137613.10:2002JAN18	152	415	forward 2	Dynein_light	Dynein light chain type 1	7.40E-20
26	LG:118836.26:2002JAN18	1084	1770	forward 1	DDHD	DDHD domain	1.10E-42
27	LG:1330261.32:2002JAN18	5538	5615	forward 3	calponin	Calponin family repeat	4.20E-11
27	LG:1330261.32:2002JAN18	5109	5441	forward 3	CH	Calponin homology (CH) domain	1.30E-06
28	LG:1347461.28:2002JAN18	864	1385	forward 3	DUF152	Uncharacterized ACR, YfiH family COG1496	6.90E-07
29	LG:1383494.16:2002JAN18	219	890	forward 3	EMP24_GP25L	emp24/gp25L/p24 family	9.90E-15
30	LG:1400155.1:2002JAN18	164	1408	forward 2	aldehyd	Aldehyde dehydrogenase family	1.90E-115
31	LG:1446621.1:2002JAN18	777	899	forward 3	KRAB	KRAB box	4.00E-23
32	LG:144920.1:2002JAN18	184	252	forward 1	zf-C2H2	Zinc finger, C2H2 type	3.60E-71
33	LG:1452619.1:2002JAN18	179	403	forward 2	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	2.90E-50
34	LG:1453417.6:2002JAN18	2374	2643	forward 1	cadherin	Cadherin domain	1.10E-76
34	LG:1453417.6:2002JAN18	7342	8073	forward 1	7tm_2	7 transmembrane receptor (Secretin family)	4.00E-57
34	LG:1453417.6:2002JAN18	3919	4080	forward 1	EGF	EGF-like domain	4.30E-31
34	LG:1453417.6:2002JAN18	7168	7329	forward 1	GPS	Latrophilin/CL-1-like GPS domain	1.50E-27
34	LG:1453417.6:2002JAN18	4408	4896	forward 1	laminin_G	Laminin G domain	4.60E-18
34	LG:1453417.6:2002JAN18	6142	6315	forward 1	HRM	Hormone receptor domain	1.60E-17
34	LG:1453417.6:2002JAN18	1436	1714	forward 2	cadherin	Cadherin domain	2.20E-81
34	LG:1453417.6:2002JAN18	780	1064	forward 3	cadherin	Cadherin domain	8.10E-27
35	LG:148485.8:2002JAN18	64	852	forward 1	FGGY	FGGY family of carbohydrate kinases, N-terminal domain	2.70E-45
35	LG:148485.8:2002JAN18	859	1551	forward 1	FGGY_C	FGGY family of carbohydrate kinases, C-terminal domain	1.10E-25
36	LG:1502670.1:2002JAN18	2	568	forward 2	arf	ADP-ribosylation factor family	1.10E-10
37	LG:206593.3:2002JAN18	307	375	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.60E-11
37	LG:206593.3:2002JAN18	476	544	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.00E-46
37	LG:206593.3:2002JAN18	54	122	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.00E-21
38	LG:228273.22:2002JAN18	877	1098	forward 1	mbt	mbt repeat	1.00E-138

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
38	LG:228273.22:2002JAN18	1801	1896	forward 1	zf-C2HC	Zinc finger, C2HC type	3.40E-11
38	LG:228273.22:2002JAN18	2194	2388	forward 1	SAM	SAM domain (Sterile alpha motif)	7.70E-08
39	LG:228319.2:2002JAN18	835	1056	forward 1	mbt	mbt repeat	9.50E-81
39	LG:228319.2:2002JAN18	1470	1679	forward 3	mbt	mbt repeat	1.60E-38
40	LG:229165.16:2002JAN18	155	1465	forward 2	P53	P53	4.00E-196
41	LG:230895.9:2002JAN18	73	627	forward 1	Glycos_transf_2	Glycosyl transferase	5.60E-37
41	LG:230895.9:2002JAN18	1012	1137	forward 1	Ricin_B_lectin	QXW lectin repeat	7.70E-35
42	LG:233552.5:2002JAN18	874	1425	forward 1	MIF4G	MIF4G domain	4.80E-37
42	LG:233552.5:2002JAN18	1750	2070	forward 1	MA3	MA3 domain	1.90E-25
43	LG:234430.7:2002JAN18	123	848	forward 3	Hydrolase	haloacid dehalogenase-like hydrolase	1.80E-21
44	LG:236659.1:2002JAN18	300	569	forward 3	bromodomain	Bromodomain	6.50E-182
44	LG:236659.1:2002JAN18	3018	3374	forward 3	BAH	BAH domain	6.60E-87
44	LG:236659.1:2002JAN18	4290	4463	forward 3	HMG_box	HMG (high mobility group) box	0.00015
45	LG:236767.26:2002JAN18	197	391	forward 2	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	1.10E-26
46	LG:237489.7:2002JAN18	424	951	forward 1	STAS	STAS domain	2.00E-20
47	LG:238218.20:2002JAN18	250	372	forward 1	KRAB	KRAB box	3.70E-14
47	LG:238218.20:2002JAN18	1225	1779	forward 1	CENP-B	CENP-B protein	0.00056
48	LG:239939.14:2002JAN18	378	875	forward 3	ras	Ras family	1.90E-30
49	LG:242288.11:2002JAN18	700	1455	forward 1	pkinese	Protein kinase domain	1.10E-62
50	LG:242491.29:2002JAN18	70	663	forward 1	EMP24_GP25L	emp24/gp25L/p24 family	3.00E-33
51	LG:243488.41:2002JAN18	198	644	forward 3	PAP2	PAP2 superfamily	1.60E-32
52	LG:247792.18:2002JAN18	569	1711	forward 2	RNB	RNB-like protein	2.40E-115
53	LG:253193.17:2002JAN18	1854	2111	forward 3	Ets	Ets-domain	1.00E-51
54	LG:257088.20:2002JAN18	3230	3328	forward 2	ank	Ankyrin repeat	7.50E-32
54	LG:257088.20:2002JAN18	3531	3629	forward 3	ank	Ankyrin repeat	2.30E-09
55	LG:265552.1:2002JAN18	242	427	forward 2	lg	Immunoglobulin domain	7.00E-10
56	LG:275355.12:2002JAN18	49	468	forward 1	ABC_tran	ABC transporter	1.50E-06
57	LG:280014.1:2002JAN18	481	1005	forward 1	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	1.10E-16
58	LG:299937.3:2002JAN18	405	518	forward 3	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	2.50E-06
58	LG:299937.3:2002JAN18	1008	1118	forward 3	zf-B_box	B-box zinc finger	0.00055



TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
59	LG:311197.3:2002JAN18	1497	1808	forward 3	PH	PH domain	1.40E-09
60	LG:321069.2:2002JAN18	544	837	forward 1	mito_carr	Mitochondrial carrier protein	7.70E-30
61	LG:330900.8:2002JAN18	965	1537	forward 2	AAA	ATPase family associated with various cellular activities (AAA)	1.10E-80
61	LG:330900.8:2002JAN18	2546	2821	forward 2	bromodomain	Bromodomain	7.60E-15
62	LG:330931.9:2002JAN18	1	60	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.60E-39
63	LG:330985.1:2002JAN18	186	1421	forward 3	Folate_carrier	Reduced folate carrier	5.00E-292
64	LG:332027.9:2002JAN18	303	1286	forward 3	Methyltransf_5	MraW methylase family	1.00E-90
65	LG:335377.8:2002JAN18	476	601	forward 2	zf-B_box	B-box zinc finger	2.50E-15
65	LG:335377.8:2002JAN18	242	391	forward 2	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.60E-12
65	LG:335377.8:2002JAN18	1671	2033	forward 3	SPRY	SPRY domain	5.60E-18
66	LG:337452.25:2002JAN18	3	590	forward 3	pkkinase	Protein kinase domain	2.80E-10
67	LG:340580.16:2002JAN18	1049	1639	forward 2	PBX	PBX domain	6.10E-31
67	LG:340580.16:2002JAN18	1643	1822	forward 2	homeobox	Homeobox domain	1.20E-17
68	LG:350272.6:2002JAN18	947	1315	forward 2	SPRY	SPRY domain	1.10E-10
69	LG:397228.1:2002JAN18	49	165	forward 1	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.10E-11
70	LG:401325.41:2002JAN18	1260	1436	forward 3	SH3	SH3 domain	0.00011
71	LG:402029.14:2002JAN18	879	1304	forward 3	Cation_ATPase_C	Cation transporting ATPase, C-terminus	4.00E-40
72	LG:407233.2:2002JAN18	366	542	forward 3	ig	Immunoglobulin domain	1.80E-20
73	LG:407346.1:2002JAN18	285	602	forward 3	CH	Calponin homology (CH) domain	5.30E-27
74	LG:407689.7:2002JAN18	81	152	forward 3	LRR	Leucine Rich Repeat	3.00E-28
74	LG:407689.7:2002JAN18	1191	1913	forward 3	PP2C	Protein phosphatase 2C	3.60E-19
75	LG:407700.1:2002JAN18	338	865	forward 2	PGAM	Phosphoglycerate mutase family	2.10E-08
76	LG:410461.92:2002JAN18	468	764	forward 3	PA	PA domain	2.50E-20
76	LG:410461.92:2002JAN18	993	1115	forward 3	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.30E-05
77	LG:411043.3:2002JAN18	287	1273	forward 2	adh_zinc	Zinc-binding dehydrogenase	1.10E-19
78	LG:438690.47:2002JAN18	550	690	forward 1	zf-CXXC	CXXC zinc finger	1.20E-15
78	LG:438690.47:2002JAN18	1526	1672	forward 2	F-box	F-box domain	2.20E-08
79	LG:444677.81:2002JAN18	652	1092	forward 1	FAA_hydrolase	Fumarylacetoacetate (FAA) hydrolase family	1.30E-29
80	LG:457464.24:2002JAN18	1202	1297	forward 2	zf-RanBP	Zn-finger in Ran binding protein and others	1.50E-11



TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
80	LG:457464.24:2002JAN18	795	1034	forward 3	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	1.10E-17
81	LG:7684793.15:2002JAN18	384	512	forward 3	zf-B_box	B-box zinc finger	6.40E-15
81	LG:7684793.15:2002JAN18	183	287	forward 3	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	2.10E-06
82	LG:7687485.1:2002JAN18	46	114	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.00E-50
83	LG:7689661.4:2002JAN18	947	1006	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.90E-44
83	LG:7689661.4:2002JAN18	74	196	forward 2	KRAB	KRAB box	9.60E-24
83	LG:7689661.4:2002JAN18	684	752	forward 3	zf-C2H2	Zinc finger, C2H2 type	5.90E-17
84	LG:7690373.1:2002JAN18	5	73	forward 2	zf-C2H2	Zinc finger, C2H2 type	7.40E-11
85	LG:7696560.1:2002JAN18	966	1064	forward 3	ank	Ankyrin repeat	1.20E-40
86	LG:7698190.26:2002JAN18	105	209	forward 3	SAP	SAP domain	9.30E-10
87	LG:7763560.12:2002JAN18	714	1598	forward 3	NAD_kinase	ATP-NAD kinase	3.90E-51
88	LG:7763587.20:2002JAN18	1979	2077	forward 2	ank	Ankyrin repeat	8.80E-44
89	LG:899263.10:2002JAN18	455	598	forward 2	RCC1	Regulator of chromosome condensation (RCC1)	1.70E-31
90	LG:977837.31:2002JAN18	610	759	forward 1	LRRCT	Leucine rich repeat C-terminal domain	7.00E-09
91	LG:978560.13:2002JAN18	1115	1183	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.80E-93
91	LG:978560.13:2002JAN18	471	593	forward 3	KRAB	KRAB box	9.90E-25
92	LG:979390.2:2002JAN18	85	207	forward 1	KRAB	KRAB box	3.00E-23
93	LG:983019.1:2002JAN18	5	550	forward 2	T-box	T-box	5.80E-106
94	LG:997202.7:2002JAN18	365	529	forward 2	SH3	SH3 domain	4.80E-15
95	LG:998756.3:2002JAN18	454	648	forward 1	zf-DHHC	DHHC zinc finger domain	9.10E-34
96	LG:103460.28:2002JAN18	740	1321	forward 2	UDG	Uracil DNA glycosylase superfamily	1.60E-24
97	LG:1501505.19:2002JAN18	1	429	forward 1	Sulfate_transp	Sulfate transporter family	0.00017
98	LG:233444.9:2002JAN18	85	810	forward 1	DUF300	Domain of unknown function	1.30E-57
98	LG:233444.9:2002JAN18	293	946	forward 2	DUF300	Domain of unknown function	1.70E-39
99	LG:234824.7:2002JAN18	1082	1150	forward 2	LRR	Leucine Rich Repeat	0.00035
99	LG:234824.7:2002JAN18	312	383	forward 3	LRR	Leucine Rich Repeat	1.70E-50
100	LG:235708.23:2002JAN18	15	566	forward 3	DUF300	Domain of unknown function	7.20E-16
101	LG:236649.14:2002JAN18	382	456	forward 1	zf-C2H2	Zinc finger, C2H2 type	0.00021
102	LG:332474.7:2002JAN18	395	469	forward 2	KRAB	KRAB box	0.00046
103	LG:335727.8:2002JAN18	275	391	forward 2	WD40	WD domain, G-beta repeat	4.20E-13

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
104	LG:481983.1:2002JAN18	414	953	forward 3	LAG1	Longevity-assurance protein (LAG1)	1.90E-64

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
10	LG:006394.31:2002JAN18	2653	2730	forward 1	SP	
10	LG:006394.31:2002JAN18	2653	2724	forward 1	SP	
10	LG:006394.31:2002JAN18	2653	2730	forward 1	SP	
10	LG:006394.31:2002JAN18	3539	3628	forward 2	SP	
10	LG:006394.31:2002JAN18	3539	3607	forward 2	SP	
10	LG:006394.31:2002JAN18	2874	2948	forward 3	SP	
11	LG:018258.1:2002JAN18	1	9		TM	Extracellular
11	LG:018258.1:2002JAN18	10	28		TM	Transmembrane
11	LG:018258.1:2002JAN18	29	278		TM	Cytosolic
11	LG:018258.1:2002JAN18	1	222		TM	Cytosolic
11	LG:018258.1:2002JAN18	223	245		TM	Transmembrane
11	LG:018258.1:2002JAN18	246	278		TM	Extracellular
11	LG:018258.1:2002JAN18	26	94	forward 2	SP	
11	LG:018258.1:2002JAN18	26	88	forward 2	SP	
11	LG:018258.1:2002JAN18	26	82	forward 2	SP	
11	LG:018258.1:2002JAN18	636	734	forward 3	SP	
11	LG:018258.1:2002JAN18	663	734	forward 3	SP	
11	LG:018258.1:2002JAN18	636	728	forward 3	SP	
11	LG:018258.1:2002JAN18	663	728	forward 3	SP	
11	LG:018258.1:2002JAN18	663	740	forward 3	SP	
11	LG:018258.1:2002JAN18	663	725	forward 3	SP	
11	LG:018258.1:2002JAN18	663	719	forward 3	SP	
11	LG:018258.1:2002JAN18	663	740	forward 3	SP	
11	LG:018258.1:2002JAN18	663	722	forward 3	SP	
12	LG:027320.5:2002JAN18	1	37		TM	Cytosolic
12	LG:027320.5:2002JAN18	38	60		TM	Transmembrane
12	LG:027320.5:2002JAN18	61	705		TM	Extracellular
12	LG:027320.5:2002JAN18	706	728		TM	Transmembrane
12	LG:027320.5:2002JAN18	729	801		TM	Cytosolic
12	LG:027320.5:2002JAN18	802	824		TM	Transmembrane
12	LG:027320.5:2002JAN18	825	843		TM	Extracellular
12	LG:027320.5:2002JAN18	844	866		TM	Transmembrane
12	LG:027320.5:2002JAN18	867	913		TM	Cytosolic
12	LG:027320.5:2002JAN18	914	936		TM	Transmembrane
12	LG:027320.5:2002JAN18	937	1089		TM	Extracellular
12	LG:027320.5:2002JAN18	1	798		TM	Extracellular
12	LG:027320.5:2002JAN18	799	821		TM	Transmembrane
12	LG:027320.5:2002JAN18	822	833		TM	Cytosolic
12	LG:027320.5:2002JAN18	834	856		TM	Transmembrane
12	LG:027320.5:2002JAN18	857	865		TM	Extracellular
12	LG:027320.5:2002JAN18	866	888		TM	Transmembrane
12	LG:027320.5:2002JAN18	889	1089		TM	Cytosolic
12	LG:027320.5:2002JAN18	1	185		TM	Cytosolic
12	LG:027320.5:2002JAN18	186	208		TM	Transmembrane
12	LG:027320.5:2002JAN18	209	230		TM	Extracellular
12	LG:027320.5:2002JAN18	231	253		TM	Transmembrane
12	LG:027320.5:2002JAN18	254	265		TM	Cytosolic
12	LG:027320.5:2002JAN18	266	288		TM	Transmembrane
12	LG:027320.5:2002JAN18	289	309		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
12	LG:027320.5:2002JAN18	310	332		TM	Transmembrane
12	LG:027320.5:2002JAN18	333	352		TM	Cytosolic
12	LG:027320.5:2002JAN18	353	375		TM	Transmembrane
12	LG:027320.5:2002JAN18	376	378		TM	Extracellular
12	LG:027320.5:2002JAN18	379	401		TM	Transmembrane
12	LG:027320.5:2002JAN18	402	772		TM	Cytosolic
12	LG:027320.5:2002JAN18	773	795		TM	Transmembrane
12	LG:027320.5:2002JAN18	796	799		TM	Extracellular
12	LG:027320.5:2002JAN18	800	822		TM	Transmembrane
12	LG:027320.5:2002JAN18	823	834		TM	Cytosolic
12	LG:027320.5:2002JAN18	835	857		TM	Transmembrane
12	LG:027320.5:2002JAN18	858	1089		TM	Extracellular
12	LG:027320.5:2002JAN18	2386	2439	forward 1	SP	
12	LG:027320.5:2002JAN18	2386	2445	forward 1	SP	
12	LG:027320.5:2002JAN18	1129	1188	forward 1	SP	
12	LG:027320.5:2002JAN18	1129	1191	forward 1	SP	
12	LG:027320.5:2002JAN18	2534	2602	forward 2	SP	
12	LG:027320.5:2002JAN18	810	869	forward 3	SP	
12	LG:027320.5:2002JAN18	810	869	forward 3	SP	
12	LG:027320.5:2002JAN18	729	779	forward 3	SP	
12	LG:027320.5:2002JAN18	810	878	forward 3	SP	
13	LG:057499.1:2002JAN18	1	772		TM	Extracellular
13	LG:057499.1:2002JAN18	773	792		TM	Transmembrane
13	LG:057499.1:2002JAN18	793	804		TM	Cytosolic
13	LG:057499.1:2002JAN18	805	827		TM	Transmembrane
13	LG:057499.1:2002JAN18	828	1209		TM	Extracellular
13	LG:057499.1:2002JAN18	1210	1232		TM	Transmembrane
13	LG:057499.1:2002JAN18	1233	1290		TM	Cytosolic
13	LG:057499.1:2002JAN18	1291	1310		TM	Transmembrane
13	LG:057499.1:2002JAN18	1311	1868		TM	Extracellular
13	LG:057499.1:2002JAN18	1869	1891		TM	Transmembrane
13	LG:057499.1:2002JAN18	1892	1937		TM	Cytosolic
13	LG:057499.1:2002JAN18	1938	1960		TM	Transmembrane
13	LG:057499.1:2002JAN18	1961	2243		TM	Extracellular
13	LG:057499.1:2002JAN18	1	933		TM	Extracellular
13	LG:057499.1:2002JAN18	934	956		TM	Transmembrane
13	LG:057499.1:2002JAN18	957	1177		TM	Cytosolic
13	LG:057499.1:2002JAN18	1178	1200		TM	Transmembrane
13	LG:057499.1:2002JAN18	1201	1209		TM	Extracellular
13	LG:057499.1:2002JAN18	1210	1232		TM	Transmembrane
13	LG:057499.1:2002JAN18	1233	1345		TM	Cytosolic
13	LG:057499.1:2002JAN18	1346	1368		TM	Transmembrane
13	LG:057499.1:2002JAN18	1369	1387		TM	Extracellular
13	LG:057499.1:2002JAN18	1388	1410		TM	Transmembrane
13	LG:057499.1:2002JAN18	1411	1429		TM	Cytosolic
13	LG:057499.1:2002JAN18	1430	1452		TM	Transmembrane
13	LG:057499.1:2002JAN18	1453	1937		TM	Extracellular
13	LG:057499.1:2002JAN18	1938	1960		TM	Transmembrane
13	LG:057499.1:2002JAN18	1961	2098		TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
13	LG:057499.1:2002JAN18	2099	2121		TM	Transmembrane
13	LG:057499.1:2002JAN18	2122	2140		TM	Extracellular
13	LG:057499.1:2002JAN18	2141	2163		TM	Transmembrane
13	LG:057499.1:2002JAN18	2164	2169		TM	Cytosolic
13	LG:057499.1:2002JAN18	2170	2192		TM	Transmembrane
13	LG:057499.1:2002JAN18	2193	2243		TM	Extracellular
13	LG:057499.1:2002JAN18	1	771		TM	Extracellular
13	LG:057499.1:2002JAN18	772	793		TM	Transmembrane
13	LG:057499.1:2002JAN18	794	958		TM	Cytosolic
13	LG:057499.1:2002JAN18	959	981		TM	Transmembrane
13	LG:057499.1:2002JAN18	982	1084		TM	Extracellular
13	LG:057499.1:2002JAN18	1085	1107		TM	Transmembrane
13	LG:057499.1:2002JAN18	1108	1200		TM	Cytosolic
13	LG:057499.1:2002JAN18	1201	1223		TM	Transmembrane
13	LG:057499.1:2002JAN18	1224	1303		TM	Extracellular
13	LG:057499.1:2002JAN18	1304	1326		TM	Transmembrane
13	LG:057499.1:2002JAN18	1327	1422		TM	Cytosolic
13	LG:057499.1:2002JAN18	1423	1445		TM	Transmembrane
13	LG:057499.1:2002JAN18	1446	1482		TM	Extracellular
13	LG:057499.1:2002JAN18	1483	1505		TM	Transmembrane
13	LG:057499.1:2002JAN18	1506	1593		TM	Cytosolic
13	LG:057499.1:2002JAN18	1594	1613		TM	Transmembrane
13	LG:057499.1:2002JAN18	1614	1627		TM	Extracellular
13	LG:057499.1:2002JAN18	1628	1650		TM	Transmembrane
13	LG:057499.1:2002JAN18	1651	1656		TM	Cytosolic
13	LG:057499.1:2002JAN18	1657	1679		TM	Transmembrane
13	LG:057499.1:2002JAN18	1680	1683		TM	Extracellular
13	LG:057499.1:2002JAN18	1684	1706		TM	Transmembrane
13	LG:057499.1:2002JAN18	1707	1799		TM	Cytosolic
13	LG:057499.1:2002JAN18	1800	1822		TM	Transmembrane
13	LG:057499.1:2002JAN18	1823	1936		TM	Extracellular
13	LG:057499.1:2002JAN18	1937	1959		TM	Transmembrane
13	LG:057499.1:2002JAN18	1960	2097		TM	Cytosolic
13	LG:057499.1:2002JAN18	2098	2120		TM	Transmembrane
13	LG:057499.1:2002JAN18	2121	2151		TM	Extracellular
13	LG:057499.1:2002JAN18	2152	2174		TM	Transmembrane
13	LG:057499.1:2002JAN18	2175	2242		TM	Cytosolic
13	LG:057499.1:2002JAN18	5782	5859	forward 1	SP	
13	LG:057499.1:2002JAN18	2329	2400	forward 1	SP	
13	LG:057499.1:2002JAN18	2329	2400	forward 1	SP	
13	LG:057499.1:2002JAN18	2329	2379	forward 1	SP	
13	LG:057499.1:2002JAN18	5809	5859	forward 1	SP	
13	LG:057499.1:2002JAN18	5809	5868	forward 1	SP	
13	LG:057499.1:2002JAN18	6303	6374	forward 3	SP	
13	LG:057499.1:2002JAN18	6297	6374	forward 3	SP	
13	LG:057499.1:2002JAN18	6312	6368	forward 3	SP	
13	LG:057499.1:2002JAN18	6294	6368	forward 3	SP	
13	LG:057499.1:2002JAN18	6303	6368	forward 3	SP	
13	LG:057499.1:2002JAN18	6312	6371	forward 3	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
14	LG:065935.21:2002JAN18	1	166		TM	Extracellular
14	LG:065935.21:2002JAN18	167	189		TM	Transmembrane
14	LG:065935.21:2002JAN18	190	201		TM	Cytosolic
14	LG:065935.21:2002JAN18	202	224		TM	Transmembrane
14	LG:065935.21:2002JAN18	225	313		TM	Extracellular
15	LG:071860.12:2002JAN18	1	49		TM	Extracellular
15	LG:071860.12:2002JAN18	50	72		TM	Transmembrane
15	LG:071860.12:2002JAN18	73	117		TM	Cytosolic
15	LG:071860.12:2002JAN18	118	140		TM	Transmembrane
15	LG:071860.12:2002JAN18	141	257		TM	Extracellular
15	LG:071860.12:2002JAN18	240	308	forward 3	SP	
15	LG:071860.12:2002JAN18	240	314	forward 3	SP	
15	LG:071860.12:2002JAN18	240	314	forward 3	SP	
15	LG:071860.12:2002JAN18	240	317	forward 3	SP	
15	LG:071860.12:2002JAN18	240	320	forward 3	SP	
16	LG:087383.29:2002JAN18	1103	1165	forward 2	SP	
16	LG:087383.29:2002JAN18	1100	1153	forward 2	SP	
16	LG:087383.29:2002JAN18	1103	1165	forward 2	SP	
17	LG:098580.3:2002JAN18	1	161		TM	Extracellular
17	LG:098580.3:2002JAN18	162	184		TM	Transmembrane
17	LG:098580.3:2002JAN18	185	221		TM	Cytosolic
17	LG:098580.3:2002JAN18	222	244		TM	Transmembrane
17	LG:098580.3:2002JAN18	245	250		TM	Extracellular
17	LG:098580.3:2002JAN18	1	168		TM	Cytosolic
17	LG:098580.3:2002JAN18	169	191		TM	Transmembrane
17	LG:098580.3:2002JAN18	192	222		TM	Extracellular
17	LG:098580.3:2002JAN18	223	245		TM	Transmembrane
17	LG:098580.3:2002JAN18	246	250		TM	Cytosolic
17	LG:098580.3:2002JAN18	1	219		TM	Cytosolic
17	LG:098580.3:2002JAN18	220	242		TM	Transmembrane
17	LG:098580.3:2002JAN18	243	250		TM	Extracellular
17	LG:098580.3:2002JAN18	504	569	forward 3	SP	
18	LG:1001879.1:2002JAN18	148	225	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	225	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	225	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	219	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	207	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	219	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	225	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	210	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	204	forward 1	SP	
19	LG:1079456.4:2002JAN18	1	218		TM	Extracellular
19	LG:1079456.4:2002JAN18	219	241		TM	Transmembrane
19	LG:1079456.4:2002JAN18	242	256		TM	Cytosolic
19	LG:1079456.4:2002JAN18	548	625	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	625	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	619	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	601	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	625	forward 2	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
19	LG:1079456.4:2002JAN18	548	613	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	610	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	610	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	619	forward 2	SP	
20	LG:1080598.9:2002JAN18	182	238	forward 2	SP	
21	LG:1090358.10:2002JAN18	1	3		TM	Extracellular
21	LG:1090358.10:2002JAN18	4	26		TM	Transmembrane
21	LG:1090358.10:2002JAN18	27	30		TM	Cytosolic
21	LG:1090358.10:2002JAN18	31	53		TM	Transmembrane
21	LG:1090358.10:2002JAN18	54	733		TM	Extracellular
21	LG:1090358.10:2002JAN18	1	3		TM	Extracellular
21	LG:1090358.10:2002JAN18	4	26		TM	Transmembrane
21	LG:1090358.10:2002JAN18	27	32		TM	Cytosolic
21	LG:1090358.10:2002JAN18	33	55		TM	Transmembrane
21	LG:1090358.10:2002JAN18	56	733		TM	Extracellular
21	LG:1090358.10:2002JAN18	1226	1285	forward 2	SP	
21	LG:1090358.10:2002JAN18	1226	1276	forward 2	SP	
21	LG:1090358.10:2002JAN18	1226	1288	forward 2	SP	
21	LG:1090358.10:2002JAN18	1226	1291	forward 2	SP	
21	LG:1090358.10:2002JAN18	692	757	forward 2	SP	
22	LG:1097492.2:2002JAN18	2941	3012	forward 1	SP	
22	LG:1097492.2:2002JAN18	2941	3012	forward 1	SP	
22	LG:1097492.2:2002JAN18	2941	3012	forward 1	SP	
22	LG:1097492.2:2002JAN18	2941	3006	forward 1	SP	
22	LG:1097492.2:2002JAN18	539	634	forward 2	SP	
22	LG:1097492.2:2002JAN18	2331	2402	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2408	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2426	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2402	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2396	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2393	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2402	forward 3	SP	
23	LG:1099945.26:2002JAN18	1	726		TM	Extracellular
23	LG:1099945.26:2002JAN18	727	744		TM	Transmembrane
23	LG:1099945.26:2002JAN18	745	842		TM	Cytosolic
23	LG:1099945.26:2002JAN18	1738	1809	forward 1	SP	
24	LG:110016.1:2002JAN18	1762	1857	forward 1	SP	
24	LG:110016.1:2002JAN18	154	258	forward 1	SP	
24	LG:110016.1:2002JAN18	740	826	forward 2	SP	
24	LG:110016.1:2002JAN18	953	1012	forward 2	SP	
24	LG:110016.1:2002JAN18	1344	1421	forward 3	SP	
24	LG:110016.1:2002JAN18	1344	1421	forward 3	SP	
25	LG:1137613.10:2002JAN18	1	874		TM	Extracellular
25	LG:1137613.10:2002JAN18	875	897		TM	Transmembrane
25	LG:1137613.10:2002JAN18	898	903		TM	Cytosolic
25	LG:1137613.10:2002JAN18	1	363		TM	Extracellular
25	LG:1137613.10:2002JAN18	364	386		TM	Transmembrane
25	LG:1137613.10:2002JAN18	387	398		TM	Cytosolic
25	LG:1137613.10:2002JAN18	399	421		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
25	LG:1137613.10:2002JAN18	422	903			
25	LG:1137613.10:2002JAN18	1	213		TM	Extracellular
25	LG:1137613.10:2002JAN18	214	236		TM	Extracellular
25	LG:1137613.10:2002JAN18	237	394		TM	Transmembrane
25	LG:1137613.10:2002JAN18	395	417		TM	Cytosolic
25	LG:1137613.10:2002JAN18	418	458		TM	Transmembrane
25	LG:1137613.10:2002JAN18	459	481		TM	Extracellular
25	LG:1137613.10:2002JAN18	482	665		TM	Transmembrane
25	LG:1137613.10:2002JAN18	666	688		TM	Cytosolic
25	LG:1137613.10:2002JAN18	689	903		TM	Transmembrane
25	LG:1137613.10:2002JAN18	2647	2706	forward 1	SP	Extracellular
25	LG:1137613.10:2002JAN18	2647	2706	forward 1	SP	
25	LG:1137613.10:2002JAN18	2647	2703	forward 1	SP	
25	LG:1137613.10:2002JAN18	2647	2700	forward 1	SP	
25	LG:1137613.10:2002JAN18	1028	1087	forward 2	SP	
25	LG:1137613.10:2002JAN18	1172	1258	forward 2	SP	
25	LG:1137613.10:2002JAN18	1028	1087	forward 2	SP	
25	LG:1137613.10:2002JAN18	1566	1655	forward 3	SP	
25	LG:1137613.10:2002JAN18	1371	1439	forward 3	SP	
25	LG:1137613.10:2002JAN18	1371	1430	forward 3	SP	
25	LG:1137613.10:2002JAN18	1371	1436	forward 3	SP	
26	LG:118836.26:2002JAN18	3778	3855	forward 1	SP	
26	LG:118836.26:2002JAN18	1529	1618	forward 2	SP	
26	LG:118836.26:2002JAN18	1529	1606	forward 2	SP	
26	LG:118836.26:2002JAN18	1529	1600	forward 2	SP	
26	LG:118836.26:2002JAN18	4940	5002	forward 2	SP	
26	LG:118836.26:2002JAN18	1529	1600	forward 2	SP	
26	LG:118836.26:2002JAN18	3791	3850	forward 2	SP	
26	LG:118836.26:2002JAN18	756	830	forward 3	SP	
26	LG:118836.26:2002JAN18	756	809	forward 3	SP	
26	LG:118836.26:2002JAN18	756	821	forward 3	SP	
26	LG:118836.26:2002JAN18	756	818	forward 3	SP	
26	LG:118836.26:2002JAN18	756	815	forward 3	SP	
26	LG:118836.26:2002JAN18	756	815	forward 3	SP	
27	LG:1330261.32:2002JAN18	1	284		TM	Extracellular
27	LG:1330261.32:2002JAN18	285	307		TM	Transmembrane
27	LG:1330261.32:2002JAN18	308	460		TM	Cytosolic
27	LG:1330261.32:2002JAN18	461	483		TM	Transmembrane
27	LG:1330261.32:2002JAN18	484	511		TM	Extracellular
27	LG:1330261.32:2002JAN18	512	534		TM	Transmembrane
27	LG:1330261.32:2002JAN18	535	559		TM	Cytosolic
27	LG:1330261.32:2002JAN18	560	582		TM	Transmembrane
27	LG:1330261.32:2002JAN18	583	616		TM	Extracellular
27	LG:1330261.32:2002JAN18	617	639		TM	Transmembrane
27	LG:1330261.32:2002JAN18	640	645		TM	Cytosolic
27	LG:1330261.32:2002JAN18	646	668		TM	Transmembrane
27	LG:1330261.32:2002JAN18	669	726		TM	Extracellular
27	LG:1330261.32:2002JAN18	727	749		TM	Transmembrane
27	LG:1330261.32:2002JAN18	750	761		TM	Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
27	LG:1330261.32:2002JAN18	762	784		TM	Transmembrane
27	LG:1330261.32:2002JAN18	785	2007		TM	Extracellular
27	LG:1330261.32:2002JAN18	2245	2325	forward 1	SP	
27	LG:1330261.32:2002JAN18	865	927	forward 1	SP	
27	LG:1330261.32:2002JAN18	2245	2325	forward 1	SP	
27	LG:1330261.32:2002JAN18	4987	5046	forward 1	SP	
27	LG:1330261.32:2002JAN18	2245	2325	forward 1	SP	
27	LG:1330261.32:2002JAN18	5104	5199	forward 1	SP	
27	LG:1330261.32:2002JAN18	1085	1144	forward 2	SP	
27	LG:1330261.32:2002JAN18	2153	2251	forward 2	SP	
27	LG:1330261.32:2002JAN18	2153	2218	forward 2	SP	
27	LG:1330261.32:2002JAN18	1052	1108	forward 2	SP	
27	LG:1330261.32:2002JAN18	1052	1126	forward 2	SP	
27	LG:1330261.32:2002JAN18	1052	1120	forward 2	SP	
28	LG:1347461.28:2002JAN18	1	1051		TM	Extracellular
28	LG:1347461.28:2002JAN18	1052	1074		TM	Transmembrane
28	LG:1347461.28:2002JAN18	1075	1085		TM	Cytosolic
28	LG:1347461.28:2002JAN18	1086	1105		TM	Transmembrane
28	LG:1347461.28:2002JAN18	1106	1150		TM	Extracellular
28	LG:1347461.28:2002JAN18	1151	1173		TM	Transmembrane
28	LG:1347461.28:2002JAN18	1174	1282		TM	Cytosolic
28	LG:1347461.28:2002JAN18	1283	1305		TM	Transmembrane
28	LG:1347461.28:2002JAN18	1306	1331		TM	Extracellular
28	LG:1347461.28:2002JAN18	364	414	forward 1	SP	
29	LG:1383494.16:2002JAN18	1	579		TM	Extracellular
29	LG:1383494.16:2002JAN18	580	602		TM	Transmembrane
29	LG:1383494.16:2002JAN18	603	712		TM	Cytosolic
29	LG:1383494.16:2002JAN18	713	735		TM	Transmembrane
29	LG:1383494.16:2002JAN18	736	962		TM	Extracellular
29	LG:1383494.16:2002JAN18	963	985		TM	Transmembrane
29	LG:1383494.16:2002JAN18	986	1048		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1049	1071		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1072	1080		TM	Extracellular
29	LG:1383494.16:2002JAN18	1081	1103		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1104	1239		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1240	1262		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1263	1276		TM	Extracellular
29	LG:1383494.16:2002JAN18	1277	1299		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1300	1441		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1442	1464		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1465	1535		TM	Extracellular
29	LG:1383494.16:2002JAN18	1536	1558		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1559	1771		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1772	1794		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1795	1800		TM	Extracellular
29	LG:1383494.16:2002JAN18	1	1049		TM	Extracellular
29	LG:1383494.16:2002JAN18	1050	1072		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1073	1073		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1074	1096		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
29	LG:1383494.16:2002JAN18	1097	1115			
29	LG:1383494.16:2002JAN18	1116	1138		TM	Extracellular
29	LG:1383494.16:2002JAN18	1139	1144		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1145	1164		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1165	1253		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1254	1276		TM	Extracellular
29	LG:1383494.16:2002JAN18	1277	1282		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1283	1305		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1306	1533		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1534	1556		TM	Extracellular
29	LG:1383494.16:2002JAN18	1557	1800		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1	263		TM	Cytosolic
29	LG:1383494.16:2002JAN18	264	286		TM	Cytosolic
29	LG:1383494.16:2002JAN18	287	690		TM	Transmembrane
29	LG:1383494.16:2002JAN18	691	709		TM	Extracellular
29	LG:1383494.16:2002JAN18	710	721		TM	Transmembrane
29	LG:1383494.16:2002JAN18	722	744		TM	Cytosolic
29	LG:1383494.16:2002JAN18	745	785		TM	Transmembrane
29	LG:1383494.16:2002JAN18	786	808		TM	Extracellular
29	LG:1383494.16:2002JAN18	809	957		TM	Transmembrane
29	LG:1383494.16:2002JAN18	958	980		TM	Cytosolic
29	LG:1383494.16:2002JAN18	981	983		TM	Transmembrane
29	LG:1383494.16:2002JAN18	984	1003		TM	Extracellular
29	LG:1383494.16:2002JAN18	1004	1046		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1047	1069		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1070	1078		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1079	1101		TM	Extracellular
29	LG:1383494.16:2002JAN18	1102	1121		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1122	1144		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1145	1799		TM	Transmembrane
29	LG:1383494.16:2002JAN18	139	225	forward 1	SP	Extracellular
29	LG:1383494.16:2002JAN18	139	225	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	219	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	210	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	213	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	207	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	198	forward 1	SP	
29	LG:1383494.16:2002JAN18	145	207	forward 1	SP	
29	LG:1383494.16:2002JAN18	4595	4648	forward 2	SP	
29	LG:1383494.16:2002JAN18	4595	4654	forward 2	SP	
29	LG:1383494.16:2002JAN18	4595	4651	forward 2	SP	
29	LG:1383494.16:2002JAN18	1692	1751	forward 3	SP	
29	LG:1383494.16:2002JAN18	1692	1754	forward 3	SP	
30	LG:1400155.1:2002JAN18	1	1563		TM	Extracellular
30	LG:1400155.1:2002JAN18	1564	1586		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1587	1644		TM	Cytosolic
30	LG:1400155.1:2002JAN18	1	1041		TM	Extracellular
30	LG:1400155.1:2002JAN18	1042	1064		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1065	1201		TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
30	LG:1400155.1:2002JAN18	1202	1224		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1225	1489		TM	Extracellular
30	LG:1400155.1:2002JAN18	1490	1512		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1513	1558		TM	Cytosolic
30	LG:1400155.1:2002JAN18	1559	1581		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1582	1595		TM	Extracellular
30	LG:1400155.1:2002JAN18	1596	1618		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1619	1644		TM	Cytosolic
30	LG:1400155.1:2002JAN18	1	1475		TM	Extracellular
30	LG:1400155.1:2002JAN18	1476	1498		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1499	1552		TM	Cytosolic
30	LG:1400155.1:2002JAN18	1553	1575		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1576	1604		TM	Extracellular
30	LG:1400155.1:2002JAN18	1605	1624		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1625	1643		TM	Cytosolic
30	LG:1400155.1:2002JAN18	2168	2245	forward 2	SP	
30	LG:1400155.1:2002JAN18	2168	2245	forward 2	SP	
30	LG:1400155.1:2002JAN18	2339	2443	forward 2	SP	
30	LG:1400155.1:2002JAN18	2168	2242	forward 2	SP	
30	LG:1400155.1:2002JAN18	2187	2255	forward 3	SP	
30	LG:1400155.1:2002JAN18	2187	2249	forward 3	SP	
30	LG:1400155.1:2002JAN18	2187	2261	forward 3	SP	
30	LG:1400155.1:2002JAN18	2187	2267	forward 3	SP	
30	LG:1400155.1:2002JAN18	2187	2240	forward 3	SP	
31	LG:1446621.1:2002JAN18	1	19		TM	Cytosolic
31	LG:1446621.1:2002JAN18	20	42		TM	Transmembrane
31	LG:1446621.1:2002JAN18	43	353		TM	Extracellular
32	LG:144920.1:2002JAN18	1376	1432	forward 2	SP	
32	LG:144920.1:2002JAN18	1376	1438	forward 2	SP	
32	LG:144920.1:2002JAN18	1376	1435	forward 2	SP	
33	LG:1452619.1:2002JAN18	1	6		TM	Cytosolic
33	LG:1452619.1:2002JAN18	7	29		TM	Transmembrane
33	LG:1452619.1:2002JAN18	30	591		TM	Extracellular
33	LG:1452619.1:2002JAN18	592	614		TM	Transmembrane
33	LG:1452619.1:2002JAN18	615	806		TM	Cytosolic
33	LG:1452619.1:2002JAN18	807	829		TM	Transmembrane
33	LG:1452619.1:2002JAN18	830	838		TM	Extracellular
33	LG:1452619.1:2002JAN18	839	861		TM	Transmembrane
33	LG:1452619.1:2002JAN18	862	872		TM	Cytosolic
33	LG:1452619.1:2002JAN18	873	895		TM	Transmembrane
33	LG:1452619.1:2002JAN18	896	1275		TM	Extracellular
33	LG:1452619.1:2002JAN18	1276	1295		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1296	1323		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1324	1346		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1347	1392		TM	Extracellular
33	LG:1452619.1:2002JAN18	1393	1412		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1413	1588		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1	589		TM	Extracellular
33	LG:1452619.1:2002JAN18	590	612		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
33	LG:1452619.1:2002JAN18	613	803		TM	Cytosolic
33	LG:1452619.1:2002JAN18	804	826		TM	Transmembrane
33	LG:1452619.1:2002JAN18	827	835		TM	Extracellular
33	LG:1452619.1:2002JAN18	836	858		TM	Transmembrane
33	LG:1452619.1:2002JAN18	859	1329		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1330	1352		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1353	1388		TM	Extracellular
33	LG:1452619.1:2002JAN18	1389	1411		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1412	1417		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1418	1437		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1438	1506		TM	Extracellular
33	LG:1452619.1:2002JAN18	1507	1526		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1527	1587		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1	588		TM	Extracellular
33	LG:1452619.1:2002JAN18	589	611		TM	Transmembrane
33	LG:1452619.1:2002JAN18	612	647		TM	Cytosolic
33	LG:1452619.1:2002JAN18	648	670		TM	Transmembrane
33	LG:1452619.1:2002JAN18	671	679		TM	Extracellular
33	LG:1452619.1:2002JAN18	680	697		TM	Transmembrane
33	LG:1452619.1:2002JAN18	698	759		TM	Cytosolic
33	LG:1452619.1:2002JAN18	760	782		TM	Transmembrane
33	LG:1452619.1:2002JAN18	783	801		TM	Extracellular
33	LG:1452619.1:2002JAN18	802	824		TM	Transmembrane
33	LG:1452619.1:2002JAN18	825	1270		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1271	1293		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1294	1296		TM	Extracellular
33	LG:1452619.1:2002JAN18	1297	1314		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1315	1330		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1331	1353		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1354	1476		TM	Extracellular
33	LG:1452619.1:2002JAN18	1477	1499		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1500	1587		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1780	1851	forward 1	SP	
33	LG:1452619.1:2002JAN18	3805	3888	forward 1	SP	
33	LG:1452619.1:2002JAN18	3043	3099	forward 1	SP	
33	LG:1452619.1:2002JAN18	902	946	forward 2	SP	
33	LG:1452619.1:2002JAN18	902	952	forward 2	SP	
33	LG:1452619.1:2002JAN18	902	964	forward 2	SP	
33	LG:1452619.1:2002JAN18	884	955	forward 2	SP	
33	LG:1452619.1:2002JAN18	2111	2176	forward 2	SP	
33	LG:1452619.1:2002JAN18	884	982	forward 2	SP	
33	LG:1452619.1:2002JAN18	902	982	forward 2	SP	
33	LG:1452619.1:2002JAN18	2274	2342	forward 3	SP	
33	LG:1452619.1:2002JAN18	2253	2342	forward 3	SP	
34	LG:1453417.6:2002JAN18	1	2453		TM	Extracellular
34	LG:1453417.6:2002JAN18	2454	2476		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2477	2488		TM	Cytosolic
34	LG:1453417.6:2002JAN18	2489	2508		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2509	2511		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
34	LG:1453417.6:2002JAN18	2512	2534		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2535	2554		TM	Cytosolic
34	LG:1453417.6:2002JAN18	2555	2574		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2575	2593		TM	Extracellular
34	LG:1453417.6:2002JAN18	2594	2616		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2617	2635		TM	Cytosolic
34	LG:1453417.6:2002JAN18	2636	2658		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2659	3378		TM	Extracellular
34	LG:1453417.6:2002JAN18	3379	3401		TM	Transmembrane
34	LG:1453417.6:2002JAN18	3402	3533		TM	Cytosolic
34	LG:1453417.6:2002JAN18	3534	3556		TM	Transmembrane
34	LG:1453417.6:2002JAN18	3557	3564		TM	Extracellular
34	LG:1453417.6:2002JAN18	1	3534		TM	Extracellular
34	LG:1453417.6:2002JAN18	3535	3557		TM	Transmembrane
34	LG:1453417.6:2002JAN18	3558	3564		TM	Cytosolic
34	LG:1453417.6:2002JAN18	223	324	forward 1	SP	
34	LG:1453417.6:2002JAN18	247	324	forward 1	SP	
34	LG:1453417.6:2002JAN18	259	321	forward 1	SP	
34	LG:1453417.6:2002JAN18	265	318	forward 1	SP	
34	LG:1453417.6:2002JAN18	265	324	forward 1	SP	
34	LG:1453417.6:2002JAN18	7675	7722	forward 1	SP	
34	LG:1453417.6:2002JAN18	5108	5215	forward 2	SP	
34	LG:1453417.6:2002JAN18	4172	4237	forward 2	SP	
34	LG:1453417.6:2002JAN18	7643	7717	forward 2	SP	
34	LG:1453417.6:2002JAN18	7643	7717	forward 2	SP	
34	LG:1453417.6:2002JAN18	5567	5626	forward 2	SP	
34	LG:1453417.6:2002JAN18	7643	7702	forward 2	SP	
34	LG:1453417.6:2002JAN18	1803	1856	forward 3	SP	
35	LG:148485.8:2002JAN18	1	694		TM	Extracellular
35	LG:148485.8:2002JAN18	695	717		TM	Transmembrane
35	LG:148485.8:2002JAN18	718	801		TM	Cytosolic
35	LG:148485.8:2002JAN18	802	824		TM	Transmembrane
35	LG:148485.8:2002JAN18	825	838		TM	Extracellular
35	LG:148485.8:2002JAN18	839	861		TM	Transmembrane
35	LG:148485.8:2002JAN18	862	941		TM	Cytosolic
35	LG:148485.8:2002JAN18	942	964		TM	Transmembrane
35	LG:148485.8:2002JAN18	965	967		TM	Extracellular
35	LG:148485.8:2002JAN18	968	990		TM	Transmembrane
35	LG:148485.8:2002JAN18	991	1069		TM	Cytosolic
35	LG:148485.8:2002JAN18	1070	1089		TM	Transmembrane
35	LG:148485.8:2002JAN18	1090	1114		TM	Extracellular
35	LG:148485.8:2002JAN18	1	20		TM	Cytosolic
35	LG:148485.8:2002JAN18	21	39		TM	Transmembrane
35	LG:148485.8:2002JAN18	40	53		TM	Extracellular
35	LG:148485.8:2002JAN18	54	76		TM	Transmembrane
35	LG:148485.8:2002JAN18	77	192		TM	Cytosolic
35	LG:148485.8:2002JAN18	193	215		TM	Transmembrane
35	LG:148485.8:2002JAN18	216	622		TM	Extracellular
35	LG:148485.8:2002JAN18	623	645		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
35	LG:148485.8:2002JAN18	646	794		TM	Cytosolic
35	LG:148485.8:2002JAN18	795	817		TM	Transmembrane
35	LG:148485.8:2002JAN18	818	845		TM	Extracellular
35	LG:148485.8:2002JAN18	846	868		TM	Transmembrane
35	LG:148485.8:2002JAN18	869	1045		TM	Cytosolic
35	LG:148485.8:2002JAN18	1046	1065		TM	Transmembrane
35	LG:148485.8:2002JAN18	1066	1074		TM	Extracellular
35	LG:148485.8:2002JAN18	1075	1097		TM	Transmembrane
35	LG:148485.8:2002JAN18	1098	1114		TM	Cytosolic
35	LG:148485.8:2002JAN18	1	799		TM	Extracellular
35	LG:148485.8:2002JAN18	800	822		TM	Transmembrane
35	LG:148485.8:2002JAN18	823	834		TM	Cytosolic
35	LG:148485.8:2002JAN18	835	857		TM	Transmembrane
35	LG:148485.8:2002JAN18	858	946		TM	Extracellular
35	LG:148485.8:2002JAN18	947	969		TM	Transmembrane
35	LG:148485.8:2002JAN18	970	980		TM	Cytosolic
35	LG:148485.8:2002JAN18	981	1003		TM	Transmembrane
35	LG:148485.8:2002JAN18	1004	1042		TM	Extracellular
35	LG:148485.8:2002JAN18	1043	1065		TM	Transmembrane
35	LG:148485.8:2002JAN18	1066	1113		TM	Cytosolic
35	LG:148485.8:2002JAN18	2381	2452	forward 2	SP	
35	LG:148485.8:2002JAN18	1373	1465	forward 2	SP	
35	LG:148485.8:2002JAN18	1373	1474	forward 2	SP	
35	LG:148485.8:2002JAN18	2381	2446	forward 2	SP	
36	LG:1502670.1:2002JAN18	293	376	forward 2	SP	
36	LG:1502670.1:2002JAN18	293	382	forward 2	SP	
36	LG:1502670.1:2002JAN18	293	364	forward 2	SP	
36	LG:1502670.1:2002JAN18	293	382	forward 2	SP	
37	LG:206593.3:2002JAN18	1	464		TM	Extracellular
37	LG:206593.3:2002JAN18	465	484		TM	Transmembrane
37	LG:206593.3:2002JAN18	485	516		TM	Cytosolic
37	LG:206593.3:2002JAN18	1364	1462	forward 2	SP	
38	LG:228273.22:2002JAN18	1	924		TM	Extracellular
38	LG:228273.22:2002JAN18	925	947		TM	Transmembrane
38	LG:228273.22:2002JAN18	948	959		TM	Cytosolic
38	LG:228273.22:2002JAN18	960	982		TM	Transmembrane
38	LG:228273.22:2002JAN18	983	1804		TM	Extracellular
38	LG:228273.22:2002JAN18	1	1643		TM	Extracellular
38	LG:228273.22:2002JAN18	1644	1666		TM	Transmembrane
38	LG:228273.22:2002JAN18	1667	1803		TM	Cytosolic
38	LG:228273.22:2002JAN18	2863	2949	forward 1	SP	
38	LG:228273.22:2002JAN18	3875	3934	forward 2	SP	
39	LG:228319.2:2002JAN18	1	305		TM	Extracellular
39	LG:228319.2:2002JAN18	306	328		TM	Transmembrane
39	LG:228319.2:2002JAN18	329	410		TM	Cytosolic
39	LG:228319.2:2002JAN18	411	433		TM	Transmembrane
39	LG:228319.2:2002JAN18	434	585		TM	Extracellular
39	LG:228319.2:2002JAN18	90	152	forward 3	SP	
39	LG:228319.2:2002JAN18	90	143	forward 3	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
39	LG:228319.2:2002JAN18	90	149	forward 3	SP	
39	LG:228319.2:2002JAN18	90	158	forward 3	SP	
39	LG:228319.2:2002JAN18	39	125	forward 3	SP	
40	LG:229165.16:2002JAN18	1	1023		TM	Extracellular
40	LG:229165.16:2002JAN18	1024	1046		TM	Transmembrane
40	LG:229165.16:2002JAN18	1047	1271		TM	Cytosolic
40	LG:229165.16:2002JAN18	1272	1294		TM	Transmembrane
40	LG:229165.16:2002JAN18	1295	1535		TM	Extracellular
40	LG:229165.16:2002JAN18	1536	1558		TM	Transmembrane
40	LG:229165.16:2002JAN18	1559	1569		TM	Cytosolic
40	LG:229165.16:2002JAN18	1570	1587		TM	Transmembrane
40	LG:229165.16:2002JAN18	1588	1616		TM	Extracellular
40	LG:229165.16:2002JAN18	1	806		TM	Extracellular
40	LG:229165.16:2002JAN18	807	826		TM	Transmembrane
40	LG:229165.16:2002JAN18	827	838		TM	Cytosolic
40	LG:229165.16:2002JAN18	839	861		TM	Transmembrane
40	LG:229165.16:2002JAN18	862	1525		TM	Extracellular
40	LG:229165.16:2002JAN18	1526	1545		TM	Transmembrane
40	LG:229165.16:2002JAN18	1546	1564		TM	Cytosolic
40	LG:229165.16:2002JAN18	1565	1587		TM	Transmembrane
40	LG:229165.16:2002JAN18	1588	1616		TM	Extracellular
40	LG:229165.16:2002JAN18	1	735		TM	Extracellular
40	LG:229165.16:2002JAN18	736	755		TM	Transmembrane
40	LG:229165.16:2002JAN18	756	775		TM	Cytosolic
40	LG:229165.16:2002JAN18	776	798		TM	Transmembrane
40	LG:229165.16:2002JAN18	799	828		TM	Extracellular
40	LG:229165.16:2002JAN18	829	851		TM	Transmembrane
40	LG:229165.16:2002JAN18	852	862		TM	Cytosolic
40	LG:229165.16:2002JAN18	863	885		TM	Transmembrane
40	LG:229165.16:2002JAN18	886	899		TM	Extracellular
40	LG:229165.16:2002JAN18	900	931		TM	Transmembrane
40	LG:229165.16:2002JAN18	932	1270		TM	Cytosolic
40	LG:229165.16:2002JAN18	1271	1293		TM	Transmembrane
40	LG:229165.16:2002JAN18	1294	1302		TM	Extracellular
40	LG:229165.16:2002JAN18	1303	1320		TM	Transmembrane
40	LG:229165.16:2002JAN18	1321	1507		TM	Cytosolic
40	LG:229165.16:2002JAN18	1508	1530		TM	Transmembrane
40	LG:229165.16:2002JAN18	1531	1563		TM	Extracellular
40	LG:229165.16:2002JAN18	1564	1586		TM	Transmembrane
40	LG:229165.16:2002JAN18	1587	1615		TM	Cytosolic
40	LG:229165.16:2002JAN18	2080	2166	forward 1	SP	
40	LG:229165.16:2002JAN18	4676	4753	forward 2	SP	
40	LG:229165.16:2002JAN18	4676	4747	forward 2	SP	
40	LG:229165.16:2002JAN18	4676	4753	forward 2	SP	
40	LG:229165.16:2002JAN18	4698	4772	forward 3	SP	
40	LG:229165.16:2002JAN18	4698	4754	forward 3	SP	
40	LG:229165.16:2002JAN18	4698	4757	forward 3	SP	
40	LG:229165.16:2002JAN18	4698	4778	forward 3	SP	
40	LG:229165.16:2002JAN18	4698	4778	forward 3	SP	



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
40	LG:229165.16:2002JAN18	1404	1496	forward 3	SP	
41	LG:230895.9:2002JAN18	1	138		TM	Cytosolic
41	LG:230895.9:2002JAN18	139	161		TM	Transmembrane
41	LG:230895.9:2002JAN18	162	596		TM	Extracellular
41	LG:230895.9:2002JAN18	749	820	forward 2	SP	
41	LG:230895.9:2002JAN18	749	826	forward 2	SP	
41	LG:230895.9:2002JAN18	749	820	forward 2	SP	
41	LG:230895.9:2002JAN18	749	814	forward 2	SP	
41	LG:230895.9:2002JAN18	749	826	forward 2	SP	
42	LG:233552.5:2002JAN18	1	1187		TM	Extracellular
42	LG:233552.5:2002JAN18	1188	1210		TM	Transmembrane
42	LG:233552.5:2002JAN18	1211	1228		TM	Cytosolic
42	LG:233552.5:2002JAN18	1	793		TM	Extracellular
42	LG:233552.5:2002JAN18	794	816		TM	Transmembrane
42	LG:233552.5:2002JAN18	817	1132		TM	Cytosolic
42	LG:233552.5:2002JAN18	1133	1152		TM	Transmembrane
42	LG:233552.5:2002JAN18	1153	1161		TM	Extracellular
42	LG:233552.5:2002JAN18	1162	1184		TM	Transmembrane
42	LG:233552.5:2002JAN18	1185	1204		TM	Cytosolic
42	LG:233552.5:2002JAN18	1205	1227		TM	Transmembrane
42	LG:233552.5:2002JAN18	1228	1228		TM	Extracellular
42	LG:233552.5:2002JAN18	3379	3432	forward 1	SP	
42	LG:233552.5:2002JAN18	3601	3645	forward 1	SP	
42	LG:233552.5:2002JAN18	719	802	forward 2	SP	
42	LG:233552.5:2002JAN18	746	808	forward 2	SP	
42	LG:233552.5:2002JAN18	746	814	forward 2	SP	
42	LG:233552.5:2002JAN18	719	820	forward 2	SP	
42	LG:233552.5:2002JAN18	170	223	forward 2	SP	
42	LG:233552.5:2002JAN18	170	229	forward 2	SP	
43	LG:234430.7:2002JAN18	2233	2298	forward 1	SP	
43	LG:234430.7:2002JAN18	2233	2292	forward 1	SP	
43	LG:234430.7:2002JAN18	2233	2346	forward 1	SP	
43	LG:234430.7:2002JAN18	1817	1894	forward 2	SP	
43	LG:234430.7:2002JAN18	1817	1894	forward 2	SP	
43	LG:234430.7:2002JAN18	1874	1945	forward 2	SP	
44	LG:236659.1:2002JAN18	1	155		TM	Cytosolic
44	LG:236659.1:2002JAN18	156	178		TM	Transmembrane
44	LG:236659.1:2002JAN18	179	1635		TM	Extracellular
44	LG:236659.1:2002JAN18	1636	1658		TM	Transmembrane
44	LG:236659.1:2002JAN18	1659	1678		TM	Cytosolic
44	LG:236659.1:2002JAN18	1679	1701		TM	Transmembrane
44	LG:236659.1:2002JAN18	1702	1715		TM	Extracellular
44	LG:236659.1:2002JAN18	1716	1734		TM	Transmembrane
44	LG:236659.1:2002JAN18	1735	1740		TM	Cytosolic
44	LG:236659.1:2002JAN18	1741	1760		TM	Transmembrane
44	LG:236659.1:2002JAN18	1761	1794		TM	Extracellular
44	LG:236659.1:2002JAN18	1795	1817		TM	Transmembrane
44	LG:236659.1:2002JAN18	1818	1873		TM	Cytosolic
44	LG:236659.1:2002JAN18	1874	1893		TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
44	LG:236659.1:2002JAN18	1894	2001		TM	Extracellular
44	LG:236659.1:2002JAN18	2002	2024		TM	Transmembrane
44	LG:236659.1:2002JAN18	2025	2093		TM	Cytosolic
44	LG:236659.1:2002JAN18	2094	2116		TM	Transmembrane
44	LG:236659.1:2002JAN18	2117	2334		TM	Extracellular
44	LG:236659.1:2002JAN18	2335	2357		TM	Transmembrane
44	LG:236659.1:2002JAN18	2358	2377		TM	Cytosolic
44	LG:236659.1:2002JAN18	2378	2395		TM	Transmembrane
44	LG:236659.1:2002JAN18	2396	2440		TM	Extracellular
44	LG:236659.1:2002JAN18	2441	2459		TM	Transmembrane
44	LG:236659.1:2002JAN18	2460	2495		TM	Cytosolic
44	LG:236659.1:2002JAN18	2496	2518		TM	Transmembrane
44	LG:236659.1:2002JAN18	2519	2915		TM	Extracellular
44	LG:236659.1:2002JAN18	1	1676		TM	Extracellular
44	LG:236659.1:2002JAN18	1677	1696		TM	Transmembrane
44	LG:236659.1:2002JAN18	1697	1708		TM	Cytosolic
44	LG:236659.1:2002JAN18	1709	1731		TM	Transmembrane
44	LG:236659.1:2002JAN18	1732	1740		TM	Extracellular
44	LG:236659.1:2002JAN18	1741	1760		TM	Transmembrane
44	LG:236659.1:2002JAN18	1761	1780		TM	Cytosolic
44	LG:236659.1:2002JAN18	1781	1803		TM	Transmembrane
44	LG:236659.1:2002JAN18	1804	2473		TM	Extracellular
44	LG:236659.1:2002JAN18	2474	2496		TM	Transmembrane
44	LG:236659.1:2002JAN18	2497	2502		TM	Cytosolic
44	LG:236659.1:2002JAN18	2503	2525		TM	Transmembrane
44	LG:236659.1:2002JAN18	2526	2914		TM	Extracellular
44	LG:236659.1:2002JAN18	1	1736		TM	Extracellular
44	LG:236659.1:2002JAN18	1737	1759		TM	Transmembrane
44	LG:236659.1:2002JAN18	1760	1993		TM	Cytosolic
44	LG:236659.1:2002JAN18	1994	2016		TM	Transmembrane
44	LG:236659.1:2002JAN18	2017	2020		TM	Extracellular
44	LG:236659.1:2002JAN18	2021	2038		TM	Transmembrane
44	LG:236659.1:2002JAN18	2039	2335		TM	Cytosolic
44	LG:236659.1:2002JAN18	2336	2358		TM	Transmembrane
44	LG:236659.1:2002JAN18	2359	2914		TM	Extracellular
44	LG:236659.1:2002JAN18	5200	5262	forward 1	SP	
44	LG:236659.1:2002JAN18	3833	3895	forward 2	SP	
44	LG:236659.1:2002JAN18	6732	6797	forward 3	SP	
44	LG:236659.1:2002JAN18	1026	1106	forward 3	SP	
44	LG:236659.1:2002JAN18	1026	1100	forward 3	SP	
45	LG:236767.26:2002JAN18	1118	1189	forward 2	SP	
45	LG:236767.26:2002JAN18	1118	1195	forward 2	SP	
45	LG:236767.26:2002JAN18	1118	1189	forward 2	SP	
45	LG:236767.26:2002JAN18	1118	1183	forward 2	SP	
46	LG:237489.7:2002JAN18	1	70		TM	Extracellular
46	LG:237489.7:2002JAN18	71	93		TM	Transmembrane
46	LG:237489.7:2002JAN18	94	94		TM	Cytosolic
46	LG:237489.7:2002JAN18	95	117		TM	Transmembrane
46	LG:237489.7:2002JAN18	118	1144		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
46	LG:237489.7:2002JAN18	1	1123		TM	Extracellular
46	LG:237489.7:2002JAN18	1124	1143		TM	Transmembrane
46	LG:237489.7:2002JAN18	1144	1144		TM	Cytosolic
46	LG:237489.7:2002JAN18	1	1113		TM	Extracellular
46	LG:237489.7:2002JAN18	1114	1136		TM	Transmembrane
46	LG:237489.7:2002JAN18	1137	1143		TM	Cytosolic
46	LG:237489.7:2002JAN18	1096	1152	forward 1	SP	
46	LG:237489.7:2002JAN18	1568	1684	forward 2	SP	
46	LG:237489.7:2002JAN18	2484	2564	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2558	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2567	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2555	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2573	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2549	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2564	forward 3	SP	
47	LG:238218.20:2002JAN18	1	794		TM	Extracellular
47	LG:238218.20:2002JAN18	795	817		TM	Transmembrane
47	LG:238218.20:2002JAN18	818	1053		TM	Cytosolic
47	LG:238218.20:2002JAN18	1054	1076		TM	Transmembrane
47	LG:238218.20:2002JAN18	1077	1090		TM	Extracellular
47	LG:238218.20:2002JAN18	1091	1113		TM	Transmembrane
47	LG:238218.20:2002JAN18	1114	1265		TM	Cytosolic
47	LG:238218.20:2002JAN18	1266	1288		TM	Transmembrane
47	LG:238218.20:2002JAN18	1289	1630		TM	Extracellular
47	LG:238218.20:2002JAN18	1631	1653		TM	Transmembrane
47	LG:238218.20:2002JAN18	1654	1735		TM	Cytosolic
47	LG:238218.20:2002JAN18	1736	1758		TM	Transmembrane
47	LG:238218.20:2002JAN18	1759	1761		TM	Extracellular
47	LG:238218.20:2002JAN18	1762	1779		TM	Transmembrane
47	LG:238218.20:2002JAN18	1780	1799		TM	Cytosolic
47	LG:238218.20:2002JAN18	1800	1822		TM	Transmembrane
47	LG:238218.20:2002JAN18	1823	1836		TM	Extracellular
47	LG:238218.20:2002JAN18	1837	1859		TM	Transmembrane
47	LG:238218.20:2002JAN18	1860	2005		TM	Cytosolic
47	LG:238218.20:2002JAN18	1	1584		TM	Extracellular
47	LG:238218.20:2002JAN18	1585	1607		TM	Transmembrane
47	LG:238218.20:2002JAN18	1608	1639		TM	Cytosolic
47	LG:238218.20:2002JAN18	1640	1662		TM	Transmembrane
47	LG:238218.20:2002JAN18	1663	2005		TM	Extracellular
47	LG:238218.20:2002JAN18	1	1090		TM	Extracellular
47	LG:238218.20:2002JAN18	1091	1113		TM	Transmembrane
47	LG:238218.20:2002JAN18	1114	1142		TM	Cytosolic
47	LG:238218.20:2002JAN18	1143	1165		TM	Transmembrane
47	LG:238218.20:2002JAN18	1166	1222		TM	Extracellular
47	LG:238218.20:2002JAN18	1223	1245		TM	Transmembrane
47	LG:238218.20:2002JAN18	1246	1265		TM	Cytosolic
47	LG:238218.20:2002JAN18	1266	1288		TM	Transmembrane
47	LG:238218.20:2002JAN18	1289	1793		TM	Extracellular
47	LG:238218.20:2002JAN18	1794	1816		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
47	LG:238218.20:2002JAN18	1817	1836		TM	Cytosolic
47	LG:238218.20:2002JAN18	1837	1859		TM	Transmembrane
47	LG:238218.20:2002JAN18	1860	2005		TM	Extracellular
47	LG:238218.20:2002JAN18	3814	3900	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3879	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3891	forward 1	SP	
47	LG:238218.20:2002JAN18	4927	4980	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3891	forward 1	SP	
47	LG:238218.20:2002JAN18	4927	4974	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3885	forward 1	SP	
47	LG:238218.20:2002JAN18	4927	4989	forward 1	SP	
47	LG:238218.20:2002JAN18	4900	4992	forward 1	SP	
47	LG:238218.20:2002JAN18	4927	4980	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3885	forward 1	SP	
47	LG:238218.20:2002JAN18	518	598	forward 2	SP	
47	LG:238218.20:2002JAN18	518	598	forward 2	SP	
47	LG:238218.20:2002JAN18	518	583	forward 2	SP	
47	LG:238218.20:2002JAN18	518	586	forward 2	SP	
47	LG:238218.20:2002JAN18	518	601	forward 2	SP	
47	LG:238218.20:2002JAN18	518	565	forward 2	SP	
47	LG:238218.20:2002JAN18	518	571	forward 2	SP	
47	LG:238218.20:2002JAN18	2400	2456	forward 3	SP	
47	LG:238218.20:2002JAN18	2400	2459	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2009	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2015	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2003	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2015	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2015	forward 3	SP	
48	LG:239939.14:2002JAN18	1	3		TM	Extracellular
48	LG:239939.14:2002JAN18	4	26		TM	Transmembrane
48	LG:239939.14:2002JAN18	27	149		TM	Cytosolic
48	LG:239939.14:2002JAN18	150	169		TM	Transmembrane
48	LG:239939.14:2002JAN18	170	183		TM	Extracellular
48	LG:239939.14:2002JAN18	184	206		TM	Transmembrane
48	LG:239939.14:2002JAN18	207	379		TM	Cytosolic
48	LG:239939.14:2002JAN18	380	402		TM	Transmembrane
48	LG:239939.14:2002JAN18	403	434		TM	Extracellular
48	LG:239939.14:2002JAN18	873	926	forward 3	SP	
48	LG:239939.14:2002JAN18	873	929	forward 3	SP	
48	LG:239939.14:2002JAN18	873	956	forward 3	SP	
49	LG:242288.11:2002JAN18	973	1044	forward 1	SP	
49	LG:242288.11:2002JAN18	4097	4195	forward 2	SP	
50	LG:242491.29:2002JAN18	64	117	forward 1	SP	
50	LG:242491.29:2002JAN18	64	120	forward 1	SP	
50	LG:242491.29:2002JAN18	64	123	forward 1	SP	
50	LG:242491.29:2002JAN18	31	117	forward 1	SP	
50	LG:242491.29:2002JAN18	64	126	forward 1	SP	
50	LG:242491.29:2002JAN18	64	117	forward 1	SP	
50	LG:242491.29:2002JAN18	31	123	forward 1	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
50	LG:242491.29:2002JAN18	64	129	forward 1	SP	
50	LG:242491.29:2002JAN18	43	117	forward 1	SP	
50	LG:242491.29:2002JAN18	31	123	forward 1	SP	
51	LG:243488.41:2002JAN18	1	525		TM	Extracellular
51	LG:243488.41:2002JAN18	526	548		TM	Transmembrane
51	LG:243488.41:2002JAN18	549	655		TM	Cytosolic
51	LG:243488.41:2002JAN18	656	678		TM	Transmembrane
51	LG:243488.41:2002JAN18	679	715		TM	Extracellular
51	LG:243488.41:2002JAN18	716	735		TM	Transmembrane
51	LG:243488.41:2002JAN18	736	742		TM	Cytosolic
51	LG:243488.41:2002JAN18	1	665		TM	Extracellular
51	LG:243488.41:2002JAN18	666	688		TM	Transmembrane
51	LG:243488.41:2002JAN18	689	742		TM	Cytosolic
51	LG:243488.41:2002JAN18	361	438	forward 1	SP	
51	LG:243488.41:2002JAN18	1940	2017	forward 2	SP	
51	LG:243488.41:2002JAN18	1940	2020	forward 2	SP	
52	LG:247792.18:2002JAN18	1	1050		TM	Extracellular
52	LG:247792.18:2002JAN18	1051	1073		TM	Transmembrane
52	LG:247792.18:2002JAN18	1074	1142		TM	Cytosolic
52	LG:247792.18:2002JAN18	1930	2016	forward 1	SP	
52	LG:247792.18:2002JAN18	1930	2010	forward 1	SP	
53	LG:253193.17:2002JAN18	1	201		TM	Extracellular
53	LG:253193.17:2002JAN18	202	224		TM	Transmembrane
53	LG:253193.17:2002JAN18	225	440		TM	Cytosolic
53	LG:253193.17:2002JAN18	441	463		TM	Transmembrane
53	LG:253193.17:2002JAN18	464	771		TM	Extracellular
53	LG:253193.17:2002JAN18	1	52		TM	Cytosolic
53	LG:253193.17:2002JAN18	53	75		TM	Transmembrane
53	LG:253193.17:2002JAN18	76	84		TM	Extracellular
53	LG:253193.17:2002JAN18	85	107		TM	Transmembrane
53	LG:253193.17:2002JAN18	108	200		TM	Cytosolic
53	LG:253193.17:2002JAN18	201	223		TM	Transmembrane
53	LG:253193.17:2002JAN18	224	291		TM	Extracellular
53	LG:253193.17:2002JAN18	292	314		TM	Transmembrane
53	LG:253193.17:2002JAN18	315	371		TM	Cytosolic
53	LG:253193.17:2002JAN18	372	394		TM	Transmembrane
53	LG:253193.17:2002JAN18	395	770		TM	Extracellular
53	LG:253193.17:2002JAN18	1	20		TM	Cytosolic
53	LG:253193.17:2002JAN18	21	40		TM	Transmembrane
53	LG:253193.17:2002JAN18	41	49		TM	Extracellular
53	LG:253193.17:2002JAN18	50	72		TM	Transmembrane
53	LG:253193.17:2002JAN18	73	152		TM	Cytosolic
53	LG:253193.17:2002JAN18	153	171		TM	Transmembrane
53	LG:253193.17:2002JAN18	172	211		TM	Extracellular
53	LG:253193.17:2002JAN18	212	234		TM	Transmembrane
53	LG:253193.17:2002JAN18	235	290		TM	Cytosolic
53	LG:253193.17:2002JAN18	291	313		TM	Transmembrane
53	LG:253193.17:2002JAN18	314	770		TM	Extracellular
53	LG:253193.17:2002JAN18	1513	1578	forward 1	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
53	LG:253193.17:2002JAN18	257	322	forward 2	SP	
53	LG:253193.17:2002JAN18	257	319	forward 2	SP	
54	LG:257088.20:2002JAN18	1	20		TM	Cytosolic
54	LG:257088.20:2002JAN18	21	43		TM	Transmembrane
54	LG:257088.20:2002JAN18	44	1253		TM	Extracellular
54	LG:257088.20:2002JAN18	1028	1153	forward 2	SP	
54	LG:257088.20:2002JAN18	1028	1147	forward 2	SP	
54	LG:257088.20:2002JAN18	1937	1999	forward 2	SP	
55	LG:265552.1:2002JAN18	1	218		TM	Cytosolic
55	LG:265552.1:2002JAN18	219	238		TM	Transmembrane
55	LG:265552.1:2002JAN18	239	247		TM	Extracellular
55	LG:265552.1:2002JAN18	248	267		TM	Transmembrane
55	LG:265552.1:2002JAN18	268	341		TM	Cytosolic
55	LG:265552.1:2002JAN18	342	364		TM	Transmembrane
55	LG:265552.1:2002JAN18	365	630		TM	Extracellular
55	LG:265552.1:2002JAN18	1	163		TM	Extracellular
55	LG:265552.1:2002JAN18	164	186		TM	Transmembrane
55	LG:265552.1:2002JAN18	187	226		TM	Cytosolic
55	LG:265552.1:2002JAN18	227	249		TM	Transmembrane
55	LG:265552.1:2002JAN18	250	291		TM	Extracellular
55	LG:265552.1:2002JAN18	292	314		TM	Transmembrane
55	LG:265552.1:2002JAN18	315	629		TM	Cytosolic
55	LG:265552.1:2002JAN18	1	381		TM	Extracellular
55	LG:265552.1:2002JAN18	382	404		TM	Transmembrane
55	LG:265552.1:2002JAN18	405	483		TM	Cytosolic
55	LG:265552.1:2002JAN18	484	506		TM	Transmembrane
55	LG:265552.1:2002JAN18	507	629		TM	Extracellular
55	LG:265552.1:2002JAN18	817	867	forward 1	SP	
55	LG:265552.1:2002JAN18	683	754	forward 2	SP	
55	LG:265552.1:2002JAN18	683	742	forward 2	SP	
55	LG:265552.1:2002JAN18	683	760	forward 2	SP	
55	LG:265552.1:2002JAN18	683	748	forward 2	SP	
55	LG:265552.1:2002JAN18	683	757	forward 2	SP	
55	LG:265552.1:2002JAN18	683	745	forward 2	SP	
55	LG:265552.1:2002JAN18	683	748	forward 2	SP	
56	LG:275355.12:2002JAN18	1	386		TM	Extracellular
56	LG:275355.12:2002JAN18	387	409		TM	Transmembrane
56	LG:275355.12:2002JAN18	410	429		TM	Cytosolic
56	LG:275355.12:2002JAN18	430	452		TM	Transmembrane
56	LG:275355.12:2002JAN18	453	514		TM	Extracellular
56	LG:275355.12:2002JAN18	1	387		TM	Extracellular
56	LG:275355.12:2002JAN18	388	410		TM	Transmembrane
56	LG:275355.12:2002JAN18	411	429		TM	Cytosolic
56	LG:275355.12:2002JAN18	430	452		TM	Transmembrane
56	LG:275355.12:2002JAN18	453	513		TM	Extracellular
56	LG:275355.12:2002JAN18	1084	1155	forward 1	SP	
56	LG:275355.12:2002JAN18	1084	1161	forward 1	SP	
56	LG:275355.12:2002JAN18	1084	1161	forward 1	SP	
56	LG:275355.12:2002JAN18	86	145	forward 2	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
57	LG:280014.1:2002JAN18	1	100		TM	Extracellular
57	LG:280014.1:2002JAN18	101	123		TM	Transmembrane
57	LG:280014.1:2002JAN18	124	238		TM	Cytosolic
57	LG:280014.1:2002JAN18	239	256		TM	Transmembrane
57	LG:280014.1:2002JAN18	257	270		TM	Extracellular
57	LG:280014.1:2002JAN18	271	293		TM	Transmembrane
57	LG:280014.1:2002JAN18	294	314		TM	Cytosolic
57	LG:280014.1:2002JAN18	315	334		TM	Transmembrane
57	LG:280014.1:2002JAN18	335	335		TM	Extracellular
57	LG:280014.1:2002JAN18	1	99		TM	Extracellular
57	LG:280014.1:2002JAN18	100	122		TM	Transmembrane
57	LG:280014.1:2002JAN18	123	335		TM	Cytosolic
57	LG:280014.1:2002JAN18	457	543	forward 1	SP	
57	LG:280014.1:2002JAN18	457	537	forward 1	SP	
57	LG:280014.1:2002JAN18	457	528	forward 1	SP	
57	LG:280014.1:2002JAN18	457	528	forward 1	SP	
57	LG:280014.1:2002JAN18	457	543	forward 1	SP	
57	LG:280014.1:2002JAN18	712	765	forward 1	SP	
57	LG:280014.1:2002JAN18	457	549	forward 1	SP	
57	LG:280014.1:2002JAN18	165	239	forward 3	SP	
57	LG:280014.1:2002JAN18	165	236	forward 3	SP	
57	LG:280014.1:2002JAN18	165	236	forward 3	SP	
57	LG:280014.1:2002JAN18	165	251	forward 3	SP	
57	LG:280014.1:2002JAN18	165	242	forward 3	SP	
57	LG:280014.1:2002JAN18	267	335	forward 3	SP	
58	LG:299937.3:2002JAN18	1	790		TM	Extracellular
58	LG:299937.3:2002JAN18	791	813		TM	Transmembrane
58	LG:299937.3:2002JAN18	814	1010		TM	Cytosolic
58	LG:299937.3:2002JAN18	817	888	forward 1	SP	
58	LG:299937.3:2002JAN18	2726	2785	forward 2	SP	
59	LG:311197.3:2002JAN18	1	1547		TM	Extracellular
59	LG:311197.3:2002JAN18	1548	1570		TM	Transmembrane
59	LG:311197.3:2002JAN18	1571	1584		TM	Cytosolic
59	LG:311197.3:2002JAN18	2227	2307	forward 1	SP	
59	LG:311197.3:2002JAN18	2227	2322	forward 1	SP	
59	LG:311197.3:2002JAN18	4552	4608	forward 1	SP	
59	LG:311197.3:2002JAN18	4552	4614	forward 1	SP	
59	LG:311197.3:2002JAN18	2850	2915	forward 3	SP	
59	LG:311197.3:2002JAN18	2850	2921	forward 3	SP	
59	LG:311197.3:2002JAN18	675	761	forward 3	SP	
60	LG:321069.2:2002JAN18	1	630		TM	Extracellular
60	LG:321069.2:2002JAN18	631	653		TM	Transmembrane
60	LG:321069.2:2002JAN18	654	665		TM	Cytosolic
60	LG:321069.2:2002JAN18	666	688		TM	Transmembrane
60	LG:321069.2:2002JAN18	689	702		TM	Extracellular
60	LG:321069.2:2002JAN18	703	725		TM	Transmembrane
60	LG:321069.2:2002JAN18	726	886		TM	Cytosolic
60	LG:321069.2:2002JAN18	887	909		TM	Transmembrane
60	LG:321069.2:2002JAN18	910	1343		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
60	LG:321069.2:2002JAN18	1	634		TM	Extracellular
60	LG:321069.2:2002JAN18	635	653		TM	Transmembrane
60	LG:321069.2:2002JAN18	654	664		TM	Cytosolic
60	LG:321069.2:2002JAN18	665	687		TM	Transmembrane
60	LG:321069.2:2002JAN18	688	806		TM	Extracellular
60	LG:321069.2:2002JAN18	807	829		TM	Transmembrane
60	LG:321069.2:2002JAN18	830	1078		TM	Cytosolic
60	LG:321069.2:2002JAN18	1079	1101		TM	Transmembrane
60	LG:321069.2:2002JAN18	1102	1127		TM	Extracellular
60	LG:321069.2:2002JAN18	1128	1150		TM	Transmembrane
60	LG:321069.2:2002JAN18	1151	1343		TM	Cytosolic
60	LG:321069.2:2002JAN18	1	448		TM	Cytosolic
60	LG:321069.2:2002JAN18	449	468		TM	Transmembrane
60	LG:321069.2:2002JAN18	469	477		TM	Extracellular
60	LG:321069.2:2002JAN18	478	500		TM	Transmembrane
60	LG:321069.2:2002JAN18	501	506		TM	Cytosolic
60	LG:321069.2:2002JAN18	507	529		TM	Transmembrane
60	LG:321069.2:2002JAN18	530	630		TM	Extracellular
60	LG:321069.2:2002JAN18	631	653		TM	Transmembrane
60	LG:321069.2:2002JAN18	654	665		TM	Cytosolic
60	LG:321069.2:2002JAN18	666	688		TM	Transmembrane
60	LG:321069.2:2002JAN18	689	692		TM	Extracellular
60	LG:321069.2:2002JAN18	693	712		TM	Transmembrane
60	LG:321069.2:2002JAN18	713	1070		TM	Cytosolic
60	LG:321069.2:2002JAN18	1071	1093		TM	Transmembrane
60	LG:321069.2:2002JAN18	1094	1102		TM	Extracellular
60	LG:321069.2:2002JAN18	1103	1122		TM	Transmembrane
60	LG:321069.2:2002JAN18	1123	1128		TM	Cytosolic
60	LG:321069.2:2002JAN18	1129	1151		TM	Transmembrane
60	LG:321069.2:2002JAN18	1152	1343		TM	Extracellular
60	LG:321069.2:2002JAN18	535	600	forward 1	SP	
60	LG:321069.2:2002JAN18	535	606	forward 1	SP	
61	LG:330900.8:2002JAN18	1	1252		TM	Extracellular
61	LG:330900.8:2002JAN18	1253	1275		TM	Transmembrane
61	LG:330900.8:2002JAN18	1276	1294		TM	Cytosolic
61	LG:330900.8:2002JAN18	1295	1317		TM	Transmembrane
61	LG:330900.8:2002JAN18	1318	1326		TM	Extracellular
61	LG:330900.8:2002JAN18	1327	1349		TM	Transmembrane
61	LG:330900.8:2002JAN18	1350	1360		TM	Cytosolic
61	LG:330900.8:2002JAN18	1361	1383		TM	Transmembrane
61	LG:330900.8:2002JAN18	1384	1458		TM	Extracellular
61	LG:330900.8:2002JAN18	1459	1481		TM	Transmembrane
61	LG:330900.8:2002JAN18	1482	1501		TM	Cytosolic
61	LG:330900.8:2002JAN18	1502	1524		TM	Transmembrane
61	LG:330900.8:2002JAN18	1525	1577		TM	Extracellular
61	LG:330900.8:2002JAN18	1578	1600		TM	Transmembrane
61	LG:330900.8:2002JAN18	1601	1630		TM	Cytosolic
61	LG:330900.8:2002JAN18	1631	1653		TM	Transmembrane
61	LG:330900.8:2002JAN18	1654	1678		TM	Extracellular



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
61	LG:330900.8:2002JAN18	1	1649		TM	Extracellular
61	LG:330900.8:2002JAN18	1650	1672		TM	Transmembrane
61	LG:330900.8:2002JAN18	1673	1678		TM	Cytosolic
61	LG:330900.8:2002JAN18	1	22		TM	Extracellular
61	LG:330900.8:2002JAN18	23	45		TM	Transmembrane
61	LG:330900.8:2002JAN18	46	115		TM	Cytosolic
61	LG:330900.8:2002JAN18	116	135		TM	Transmembrane
61	LG:330900.8:2002JAN18	136	437		TM	Extracellular
61	LG:330900.8:2002JAN18	438	460		TM	Transmembrane
61	LG:330900.8:2002JAN18	461	596		TM	Cytosolic
61	LG:330900.8:2002JAN18	597	619		TM	Transmembrane
61	LG:330900.8:2002JAN18	620	633		TM	Extracellular
61	LG:330900.8:2002JAN18	634	651		TM	Transmembrane
61	LG:330900.8:2002JAN18	652	671		TM	Cytosolic
61	LG:330900.8:2002JAN18	672	694		TM	Transmembrane
61	LG:330900.8:2002JAN18	695	1356		TM	Extracellular
61	LG:330900.8:2002JAN18	1357	1376		TM	Transmembrane
61	LG:330900.8:2002JAN18	1377	1380		TM	Cytosolic
61	LG:330900.8:2002JAN18	1381	1403		TM	Transmembrane
61	LG:330900.8:2002JAN18	1404	1433		TM	Extracellular
61	LG:330900.8:2002JAN18	1434	1456		TM	Transmembrane
61	LG:330900.8:2002JAN18	1457	1476		TM	Cytosolic
61	LG:330900.8:2002JAN18	1477	1499		TM	Transmembrane
61	LG:330900.8:2002JAN18	1500	1503		TM	Extracellular
61	LG:330900.8:2002JAN18	1504	1526		TM	Transmembrane
61	LG:330900.8:2002JAN18	1527	1654		TM	Cytosolic
61	LG:330900.8:2002JAN18	1655	1672		TM	Transmembrane
61	LG:330900.8:2002JAN18	1673	1677		TM	Extracellular
61	LG:330900.8:2002JAN18	3012	3089	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3083	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3089	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3074	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3083	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3077	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3089	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3095	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3080	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3095	forward 3	SP	
61	LG:330900.8:2002JAN18	3027	3083	forward 3	SP	
62	LG:330931.9:2002JAN18	1	1400		TM	Extracellular
62	LG:330931.9:2002JAN18	1401	1423		TM	Transmembrane
62	LG:330931.9:2002JAN18	1424	1429		TM	Cytosolic
62	LG:330931.9:2002JAN18	1430	1447		TM	Transmembrane
62	LG:330931.9:2002JAN18	1448	1701		TM	Extracellular
62	LG:330931.9:2002JAN18	1702	1724		TM	Transmembrane
62	LG:330931.9:2002JAN18	1725	1816		TM	Cytosolic
62	LG:330931.9:2002JAN18	1817	1839		TM	Transmembrane
62	LG:330931.9:2002JAN18	1840	1853		TM	Extracellular
62	LG:330931.9:2002JAN18	1854	1873		TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
62	LG:330931.9:2002JAN18	1874	1950		TM	Cytosolic
62	LG:330931.9:2002JAN18	1951	1973		TM	Transmembrane
62	LG:330931.9:2002JAN18	1974	1992		TM	Extracellular
62	LG:330931.9:2002JAN18	1993	2015		TM	Transmembrane
62	LG:330931.9:2002JAN18	2016	2035		TM	Cytosolic
62	LG:330931.9:2002JAN18	1	1109		TM	Extracellular
62	LG:330931.9:2002JAN18	1110	1132		TM	Transmembrane
62	LG:330931.9:2002JAN18	1133	1144		TM	Cytosolic
62	LG:330931.9:2002JAN18	1145	1167		TM	Transmembrane
62	LG:330931.9:2002JAN18	1168	1701		TM	Extracellular
62	LG:330931.9:2002JAN18	1702	1724		TM	Transmembrane
62	LG:330931.9:2002JAN18	1725	1822		TM	Cytosolic
62	LG:330931.9:2002JAN18	1823	1845		TM	Transmembrane
62	LG:330931.9:2002JAN18	1846	1859		TM	Extracellular
62	LG:330931.9:2002JAN18	1860	1875		TM	Transmembrane
62	LG:330931.9:2002JAN18	1876	1939		TM	Cytosolic
62	LG:330931.9:2002JAN18	1940	1962		TM	Transmembrane
62	LG:330931.9:2002JAN18	1963	1996		TM	Extracellular
62	LG:330931.9:2002JAN18	1997	2019		TM	Transmembrane
62	LG:330931.9:2002JAN18	2020	2035		TM	Cytosolic
62	LG:330931.9:2002JAN18	2662	2721	forward 1	SP	
62	LG:330931.9:2002JAN18	2662	2727	forward 1	SP	
62	LG:330931.9:2002JAN18	4906	4971	forward 1	SP	
62	LG:330931.9:2002JAN18	4906	4962	forward 1	SP	
62	LG:330931.9:2002JAN18	1826	1888	forward 2	SP	
62	LG:330931.9:2002JAN18	2073	2180	forward 3	SP	
63	LG:330985.1:2002JAN18	1	106		TM	Cytosolic
63	LG:330985.1:2002JAN18	107	129		TM	Transmembrane
63	LG:330985.1:2002JAN18	130	133		TM	Extracellular
63	LG:330985.1:2002JAN18	134	156		TM	Transmembrane
63	LG:330985.1:2002JAN18	157	162		TM	Cytosolic
63	LG:330985.1:2002JAN18	163	182		TM	Transmembrane
63	LG:330985.1:2002JAN18	183	196		TM	Extracellular
63	LG:330985.1:2002JAN18	197	216		TM	Transmembrane
63	LG:330985.1:2002JAN18	217	222		TM	Cytosolic
63	LG:330985.1:2002JAN18	223	242		TM	Transmembrane
63	LG:330985.1:2002JAN18	243	308		TM	Extracellular
63	LG:330985.1:2002JAN18	309	331		TM	Transmembrane
63	LG:330985.1:2002JAN18	332	342		TM	Cytosolic
63	LG:330985.1:2002JAN18	343	365		TM	Transmembrane
63	LG:330985.1:2002JAN18	366	369		TM	Extracellular
63	LG:330985.1:2002JAN18	370	392		TM	Transmembrane
63	LG:330985.1:2002JAN18	393	398		TM	Cytosolic
63	LG:330985.1:2002JAN18	399	421		TM	Transmembrane
63	LG:330985.1:2002JAN18	422	435		TM	Extracellular
63	LG:330985.1:2002JAN18	436	458		TM	Transmembrane
63	LG:330985.1:2002JAN18	459	470		TM	Cytosolic
63	LG:330985.1:2002JAN18	471	490		TM	Transmembrane
63	LG:330985.1:2002JAN18	491	1078		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
63	LG:330985.1:2002JAN18	1798	1857	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1869	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1875	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1872	forward 1	SP	
63	LG:330985.1:2002JAN18	550	639	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1863	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1842	forward 1	SP	
63	LG:330985.1:2002JAN18	417	476	forward 3	SP	
64	LG:332027.9:2002JAN18	1	570		TM	Extracellular
64	LG:332027.9:2002JAN18	571	593		TM	Transmembrane
64	LG:332027.9:2002JAN18	594	613		TM	Cytosolic
64	LG:332027.9:2002JAN18	614	636		TM	Transmembrane
64	LG:332027.9:2002JAN18	637	655		TM	Extracellular
64	LG:332027.9:2002JAN18	656	678		TM	Transmembrane
64	LG:332027.9:2002JAN18	679	865		TM	Cytosolic
64	LG:332027.9:2002JAN18	866	888		TM	Transmembrane
64	LG:332027.9:2002JAN18	889	968		TM	Extracellular
64	LG:332027.9:2002JAN18	969	988		TM	Transmembrane
64	LG:332027.9:2002JAN18	989	1022		TM	Cytosolic
64	LG:332027.9:2002JAN18	1	449		TM	Extracellular
64	LG:332027.9:2002JAN18	450	472		TM	Transmembrane
64	LG:332027.9:2002JAN18	473	553		TM	Cytosolic
64	LG:332027.9:2002JAN18	554	576		TM	Transmembrane
64	LG:332027.9:2002JAN18	577	624		TM	Extracellular
64	LG:332027.9:2002JAN18	625	644		TM	Transmembrane
64	LG:332027.9:2002JAN18	645	859		TM	Cytosolic
64	LG:332027.9:2002JAN18	860	882		TM	Transmembrane
64	LG:332027.9:2002JAN18	883	918		TM	Extracellular
64	LG:332027.9:2002JAN18	919	941		TM	Transmembrane
64	LG:332027.9:2002JAN18	942	961		TM	Cytosolic
64	LG:332027.9:2002JAN18	962	984		TM	Transmembrane
64	LG:332027.9:2002JAN18	985	1021		TM	Extracellular
64	LG:332027.9:2002JAN18	1	750		TM	Extracellular
64	LG:332027.9:2002JAN18	751	773		TM	Transmembrane
64	LG:332027.9:2002JAN18	774	800		TM	Cytosolic
64	LG:332027.9:2002JAN18	801	823		TM	Transmembrane
64	LG:332027.9:2002JAN18	824	872		TM	Extracellular
64	LG:332027.9:2002JAN18	873	895		TM	Transmembrane
64	LG:332027.9:2002JAN18	896	948		TM	Cytosolic
64	LG:332027.9:2002JAN18	949	971		TM	Transmembrane
64	LG:332027.9:2002JAN18	972	1021		TM	Extracellular
65	LG:335377.8:2002JAN18	3010	3108	forward 1	SP	
65	LG:335377.8:2002JAN18	3010	3084	forward 1	SP	
65	LG:335377.8:2002JAN18	2090	2143	forward 2	SP	
65	LG:335377.8:2002JAN18	2883	2945	forward 3	SP	
65	LG:335377.8:2002JAN18	2883	2957	forward 3	SP	
65	LG:335377.8:2002JAN18	2883	2951	forward 3	SP	
65	LG:335377.8:2002JAN18	3030	3110	forward 3	SP	
65	LG:335377.8:2002JAN18	2883	2948	forward 3	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
66	LG:337452.25:2002JAN18	1156	1233	forward 1	SP	
66	LG:337452.25:2002JAN18	2237	2314	forward 2	SP	
66	LG:337452.25:2002JAN18	1514	1600	forward 2	SP	
67	LG:340580.16:2002JAN18	1	393		TM	Extracellular
67	LG:340580.16:2002JAN18	394	416		TM	Transmembrane
67	LG:340580.16:2002JAN18	417	422		TM	Cytosolic
67	LG:340580.16:2002JAN18	423	440		TM	Transmembrane
67	LG:340580.16:2002JAN18	441	1131		TM	Extracellular
67	LG:340580.16:2002JAN18	1132	1151		TM	Transmembrane
67	LG:340580.16:2002JAN18	1152	1685		TM	Cytosolic
67	LG:340580.16:2002JAN18	1686	1708		TM	Transmembrane
67	LG:340580.16:2002JAN18	1709	1722		TM	Extracellular
67	LG:340580.16:2002JAN18	1723	1745		TM	Transmembrane
67	LG:340580.16:2002JAN18	1746	1796		TM	Cytosolic
67	LG:340580.16:2002JAN18	1797	1819		TM	Transmembrane
67	LG:340580.16:2002JAN18	1820	1881		TM	Extracellular
67	LG:340580.16:2002JAN18	1882	1901		TM	Transmembrane
67	LG:340580.16:2002JAN18	1902	1975		TM	Cytosolic
67	LG:340580.16:2002JAN18	1976	1998		TM	Transmembrane
67	LG:340580.16:2002JAN18	1999	2288		TM	Extracellular
67	LG:340580.16:2002JAN18	2289	2311		TM	Transmembrane
67	LG:340580.16:2002JAN18	2312	2317		TM	Cytosolic
67	LG:340580.16:2002JAN18	2318	2335		TM	Transmembrane
67	LG:340580.16:2002JAN18	2336	2446		TM	Extracellular
67	LG:340580.16:2002JAN18	1	42		TM	Cytosolic
67	LG:340580.16:2002JAN18	43	61		TM	Transmembrane
67	LG:340580.16:2002JAN18	62	80		TM	Extracellular
67	LG:340580.16:2002JAN18	81	98		TM	Transmembrane
67	LG:340580.16:2002JAN18	99	197		TM	Cytosolic
67	LG:340580.16:2002JAN18	198	220		TM	Transmembrane
67	LG:340580.16:2002JAN18	221	393		TM	Extracellular
67	LG:340580.16:2002JAN18	394	416		TM	Transmembrane
67	LG:340580.16:2002JAN18	417	428		TM	Cytosolic
67	LG:340580.16:2002JAN18	429	451		TM	Transmembrane
67	LG:340580.16:2002JAN18	452	2288		TM	Extracellular
67	LG:340580.16:2002JAN18	2289	2311		TM	Transmembrane
67	LG:340580.16:2002JAN18	2312	2323		TM	Cytosolic
67	LG:340580.16:2002JAN18	2324	2346		TM	Transmembrane
67	LG:340580.16:2002JAN18	2347	2400		TM	Extracellular
67	LG:340580.16:2002JAN18	2401	2423		TM	Transmembrane
67	LG:340580.16:2002JAN18	2424	2446		TM	Cytosolic
67	LG:340580.16:2002JAN18	1	80		TM	Cytosolic
67	LG:340580.16:2002JAN18	81	103		TM	Transmembrane
67	LG:340580.16:2002JAN18	104	391		TM	Extracellular
67	LG:340580.16:2002JAN18	392	414		TM	Transmembrane
67	LG:340580.16:2002JAN18	415	426		TM	Cytosolic
67	LG:340580.16:2002JAN18	427	449		TM	Transmembrane
67	LG:340580.16:2002JAN18	450	1729		TM	Extracellular
67	LG:340580.16:2002JAN18	1730	1761		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
67	LG:340580.16:2002JAN18	1762	1791		TM	Cytosolic
67	LG:340580.16:2002JAN18	1792	1814		TM	Transmembrane
67	LG:340580.16:2002JAN18	1815	1835		TM	Extracellular
67	LG:340580.16:2002JAN18	1836	1853		TM	Transmembrane
67	LG:340580.16:2002JAN18	1854	1873		TM	Cytosolic
67	LG:340580.16:2002JAN18	1874	1896		TM	Transmembrane
67	LG:340580.16:2002JAN18	1897	1979		TM	Extracellular
67	LG:340580.16:2002JAN18	1980	2002		TM	Transmembrane
67	LG:340580.16:2002JAN18	2003	2092		TM	Cytosolic
67	LG:340580.16:2002JAN18	2093	2115		TM	Transmembrane
67	LG:340580.16:2002JAN18	2116	2286		TM	Extracellular
67	LG:340580.16:2002JAN18	2287	2309		TM	Transmembrane
67	LG:340580.16:2002JAN18	2310	2321		TM	Cytosolic
67	LG:340580.16:2002JAN18	2322	2344		TM	Transmembrane
67	LG:340580.16:2002JAN18	2345	2363		TM	Extracellular
67	LG:340580.16:2002JAN18	2364	2386		TM	Transmembrane
67	LG:340580.16:2002JAN18	2387	2392		TM	Cytosolic
67	LG:340580.16:2002JAN18	2393	2415		TM	Transmembrane
67	LG:340580.16:2002JAN18	2416	2446		TM	Extracellular
67	LG:340580.16:2002JAN18	5926	5973	forward 1	SP	
67	LG:340580.16:2002JAN18	3085	3189	forward 1	SP	
67	LG:340580.16:2002JAN18	5926	5985	forward 1	SP	
67	LG:340580.16:2002JAN18	5926	6000	forward 1	SP	
67	LG:340580.16:2002JAN18	5926	6003	forward 1	SP	
67	LG:340580.16:2002JAN18	2573	2632	forward 2	SP	
67	LG:340580.16:2002JAN18	2573	2656	forward 2	SP	
67	LG:340580.16:2002JAN18	2573	2662	forward 2	SP	
67	LG:340580.16:2002JAN18	5187	5264	forward 3	SP	
67	LG:340580.16:2002JAN18	5202	5264	forward 3	SP	
67	LG:340580.16:2002JAN18	5187	5243	forward 3	SP	
67	LG:340580.16:2002JAN18	5187	5252	forward 3	SP	
67	LG:340580.16:2002JAN18	5187	5258	forward 3	SP	
67	LG:340580.16:2002JAN18	5187	5258	forward 3	SP	
68	LG:350272.6:2002JAN18	1	649		TM	Extracellular
68	LG:350272.6:2002JAN18	650	672		TM	Transmembrane
68	LG:350272.6:2002JAN18	673	679		TM	Cytosolic
68	LG:350272.6:2002JAN18	1967	2038	forward 2	SP	
68	LG:350272.6:2002JAN18	1832	1888	forward 2	SP	
68	LG:350272.6:2002JAN18	1967	2032	forward 2	SP	
68	LG:350272.6:2002JAN18	1967	2038	forward 2	SP	
68	LG:350272.6:2002JAN18	1967	2035	forward 2	SP	
68	LG:350272.6:2002JAN18	1793	1891	forward 2	SP	
68	LG:350272.6:2002JAN18	1967	2026	forward 2	SP	
68	LG:350272.6:2002JAN18	1787	1885	forward 2	SP	
68	LG:350272.6:2002JAN18	1218	1277	forward 3	SP	
68	LG:350272.6:2002JAN18	1218	1274	forward 3	SP	
68	LG:350272.6:2002JAN18	1218	1280	forward 3	SP	
69	LG:397228.1:2002JAN18	1	106		TM	Cytosolic
70	LG:401325.41:2002JAN18	1867	1959	forward 1	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
70	LG:401325.41:2002JAN18	2546	2617	forward 2	SP	
70	LG:401325.41:2002JAN18	2546	2611	forward 2	SP	
70	LG:401325.41:2002JAN18	2546	2617	forward 2	SP	
70	LG:401325.41:2002JAN18	2546	2596	forward 2	SP	
70	LG:401325.41:2002JAN18	2666	2722	forward 2	SP	
71	LG:402029.14:2002JAN18	1	207		TM	Extracellular
71	LG:402029.14:2002JAN18	208	230		TM	Transmembrane
71	LG:402029.14:2002JAN18	231	305		TM	Cytosolic
71	LG:402029.14:2002JAN18	306	325		TM	Transmembrane
71	LG:402029.14:2002JAN18	326	339		TM	Extracellular
71	LG:402029.14:2002JAN18	340	357		TM	Transmembrane
71	LG:402029.14:2002JAN18	358	369		TM	Cytosolic
71	LG:402029.14:2002JAN18	370	392		TM	Transmembrane
71	LG:402029.14:2002JAN18	393	1147		TM	Extracellular
71	LG:402029.14:2002JAN18	2527	2607	forward 1	SP	
71	LG:402029.14:2002JAN18	1342	1431	forward 1	SP	
72	LG:407233.2:2002JAN18	1	773		TM	Extracellular
72	LG:407233.2:2002JAN18	774	796		TM	Transmembrane
72	LG:407233.2:2002JAN18	797	798		TM	Cytosolic
72	LG:407233.2:2002JAN18	1	57		TM	Cytosolic
72	LG:407233.2:2002JAN18	58	80		TM	Transmembrane
72	LG:407233.2:2002JAN18	81	798		TM	Extracellular
72	LG:407233.2:2002JAN18	1	50		TM	Extracellular
72	LG:407233.2:2002JAN18	51	73		TM	Transmembrane
72	LG:407233.2:2002JAN18	74	390		TM	Cytosolic
72	LG:407233.2:2002JAN18	391	413		TM	Transmembrane
72	LG:407233.2:2002JAN18	414	689		TM	Extracellular
72	LG:407233.2:2002JAN18	690	712		TM	Transmembrane
72	LG:407233.2:2002JAN18	713	798		TM	Cytosolic
72	LG:407233.2:2002JAN18	1180	1266	forward 1	SP	
72	LG:407233.2:2002JAN18	139	213	forward 1	SP	
72	LG:407233.2:2002JAN18	1192	1257	forward 1	SP	
72	LG:407233.2:2002JAN18	1204	1266	forward 1	SP	
72	LG:407233.2:2002JAN18	1182	1265	forward 3	SP	
73	LG:407346.1:2002JAN18	1	519		TM	Extracellular
73	LG:407346.1:2002JAN18	520	542		TM	Transmembrane
73	LG:407346.1:2002JAN18	543	562		TM	Cytosolic
73	LG:407346.1:2002JAN18	563	585		TM	Transmembrane
73	LG:407346.1:2002JAN18	586	1725		TM	Extracellular
73	LG:407346.1:2002JAN18	1726	1748		TM	Transmembrane
73	LG:407346.1:2002JAN18	1749	2071		TM	Cytosolic
73	LG:407346.1:2002JAN18	2072	2094		TM	Transmembrane
73	LG:407346.1:2002JAN18	2095	2126		TM	Extracellular
73	LG:407346.1:2002JAN18	2127	2149		TM	Transmembrane
73	LG:407346.1:2002JAN18	2150	2161		TM	Cytosolic
73	LG:407346.1:2002JAN18	1	2001		TM	Extracellular
73	LG:407346.1:2002JAN18	2002	2021		TM	Transmembrane
73	LG:407346.1:2002JAN18	2022	2161		TM	Cytosolic
73	LG:407346.1:2002JAN18	1	1616		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
73	LG:407346.1:2002JAN18	1617	1639		TM	Transmembrane
73	LG:407346.1:2002JAN18	1640	1741		TM	Cytosolic
73	LG:407346.1:2002JAN18	1742	1764		TM	Transmembrane
73	LG:407346.1:2002JAN18	1765	2161		TM	Extracellular
74	LG:407689.7:2002JAN18	1	2173		TM	Extracellular
74	LG:407689.7:2002JAN18	2174	2196		TM	Transmembrane
74	LG:407689.7:2002JAN18	2197	2202		TM	Cytosolic
74	LG:407689.7:2002JAN18	2203	2225		TM	Transmembrane
74	LG:407689.7:2002JAN18	2226	2259		TM	Extracellular
74	LG:407689.7:2002JAN18	2188	2262	forward 1	SP	
74	LG:407689.7:2002JAN18	4693	4752	forward 1	SP	
74	LG:407689.7:2002JAN18	2182	2262	forward 1	SP	
74	LG:407689.7:2002JAN18	2104	2181	forward 1	SP	
74	LG:407689.7:2002JAN18	1378	1458	forward 1	SP	
74	LG:407689.7:2002JAN18	2023	2094	forward 1	SP	
74	LG:407689.7:2002JAN18	4693	4755	forward 1	SP	
74	LG:407689.7:2002JAN18	6269	6331	forward 2	SP	
74	LG:407689.7:2002JAN18	1206	1274	forward 3	SP	
75	LG:407700.1:2002JAN18	1	20		TM	Cytosolic
75	LG:407700.1:2002JAN18	21	43		TM	Transmembrane
75	LG:407700.1:2002JAN18	44	750		TM	Extracellular
75	LG:407700.1:2002JAN18	1	571		TM	Extracellular
75	LG:407700.1:2002JAN18	572	594		TM	Transmembrane
75	LG:407700.1:2002JAN18	595	714		TM	Cytosolic
75	LG:407700.1:2002JAN18	715	737		TM	Transmembrane
75	LG:407700.1:2002JAN18	738	750		TM	Extracellular
75	LG:407700.1:2002JAN18	47	106	forward 2	SP	
75	LG:407700.1:2002JAN18	47	106	forward 2	SP	
75	LG:407700.1:2002JAN18	47	139	forward 2	SP	
75	LG:407700.1:2002JAN18	47	103	forward 2	SP	
75	LG:407700.1:2002JAN18	47	109	forward 2	SP	
75	LG:407700.1:2002JAN18	378	464	forward 3	SP	
76	LG:410461.92:2002JAN18	1	262		TM	Extracellular
76	LG:410461.92:2002JAN18	263	285		TM	Transmembrane
76	LG:410461.92:2002JAN18	286	492		TM	Cytosolic
76	LG:410461.92:2002JAN18	493	515		TM	Transmembrane
76	LG:410461.92:2002JAN18	516	950		TM	Extracellular
76	LG:410461.92:2002JAN18	258	344	forward 3	SP	
76	LG:410461.92:2002JAN18	258	344	forward 3	SP	
76	LG:410461.92:2002JAN18	258	338	forward 3	SP	
76	LG:410461.92:2002JAN18	273	344	forward 3	SP	
76	LG:410461.92:2002JAN18	273	338	forward 3	SP	
76	LG:410461.92:2002JAN18	258	338	forward 3	SP	
76	LG:410461.92:2002JAN18	276	338	forward 3	SP	
77	LG:411043.3:2002JAN18	1	121		TM	Cytosolic
77	LG:411043.3:2002JAN18	122	144		TM	Transmembrane
77	LG:411043.3:2002JAN18	145	203		TM	Extracellular
77	LG:411043.3:2002JAN18	204	223		TM	Transmembrane
77	LG:411043.3:2002JAN18	224	458		TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
77	LG:411043.3:2002JAN18	459	481		TM	Transmembrane
77	LG:411043.3:2002JAN18	482	707		TM	Extracellular
77	LG:411043.3:2002JAN18	606	668	forward 3	SP	
78	LG:438690.47:2002JAN18	1	1512		TM	Extracellular
78	LG:438690.47:2002JAN18	1513	1535		TM	Transmembrane
78	LG:438690.47:2002JAN18	1536	1767		TM	Cytosolic
78	LG:438690.47:2002JAN18	1768	1787		TM	Transmembrane
78	LG:438690.47:2002JAN18	1788	1788		TM	Extracellular
78	LG:438690.47:2002JAN18	1	1506		TM	Extracellular
78	LG:438690.47:2002JAN18	1507	1529		TM	Transmembrane
78	LG:438690.47:2002JAN18	1530	1662		TM	Cytosolic
78	LG:438690.47:2002JAN18	1663	1685		TM	Transmembrane
78	LG:438690.47:2002JAN18	1686	1788		TM	Extracellular
78	LG:438690.47:2002JAN18	3451	3522	forward 1	SP	
78	LG:438690.47:2002JAN18	1777	1866	forward 1	SP	
78	LG:438690.47:2002JAN18	3451	3522	forward 1	SP	
78	LG:438690.47:2002JAN18	3451	3525	forward 1	SP	
78	LG:438690.47:2002JAN18	3032	3085	forward 2	SP	
78	LG:438690.47:2002JAN18	3032	3091	forward 2	SP	
78	LG:438690.47:2002JAN18	1043	1120	forward 2	SP	
78	LG:438690.47:2002JAN18	3032	3100	forward 2	SP	
78	LG:438690.47:2002JAN18	582	650	forward 3	SP	
79	LG:444677.81:2002JAN18	1055	1111	forward 2	SP	
79	LG:444677.81:2002JAN18	818	880	forward 2	SP	
79	LG:444677.81:2002JAN18	234	293	forward 3	SP	
80	LG:457464.24:2002JAN18	1	438		TM	Extracellular
80	LG:457464.24:2002JAN18	439	461		TM	Transmembrane
80	LG:457464.24:2002JAN18	462	536		TM	Cytosolic
80	LG:457464.24:2002JAN18	1000	1092	forward 1	SP	
80	LG:457464.24:2002JAN18	1347	1400	forward 3	SP	
80	LG:457464.24:2002JAN18	1347	1403	forward 3	SP	
81	LG:7684793.15:2002JAN18	940	1002	forward 1	SP	
81	LG:7684793.15:2002JAN18	940	1008	forward 1	SP	
81	LG:7684793.15:2002JAN18	3253	3345	forward 1	SP	
81	LG:7684793.15:2002JAN18	3155	3244	forward 2	SP	
81	LG:7684793.15:2002JAN18	2117	2194	forward 2	SP	
81	LG:7684793.15:2002JAN18	2114	2188	forward 2	SP	
81	LG:7684793.15:2002JAN18	3984	4058	forward 3	SP	
82	LG:7687485.1:2002JAN18	1	252		TM	Cytosolic
82	LG:7687485.1:2002JAN18	253	275		TM	Transmembrane
82	LG:7687485.1:2002JAN18	276	380		TM	Extracellular
82	LG:7687485.1:2002JAN18	781	828	forward 1	SP	
82	LG:7687485.1:2002JAN18	781	834	forward 1	SP	
82	LG:7687485.1:2002JAN18	299	367	forward 2	SP	
82	LG:7687485.1:2002JAN18	299	361	forward 2	SP	
83	LG:7689661.4:2002JAN18	1	345		TM	Extracellular
83	LG:7689661.4:2002JAN18	346	365		TM	Transmembrane
83	LG:7689661.4:2002JAN18	366	509		TM	Cytosolic
83	LG:7689661.4:2002JAN18	510	532		TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
83	LG:7689661.4:2002JAN18	533	757		TM	Extracellular
83	LG:7689661.4:2002JAN18	1562	1618	forward 2	SP	
84	LG:7690373.1:2002JAN18	1	95		TM	Cytosolic
84	LG:7690373.1:2002JAN18	96	118		TM	Transmembrane
84	LG:7690373.1:2002JAN18	119	219		TM	Extracellular
85	LG:7696560.1:2002JAN18	1	556		TM	Extracellular
85	LG:7696560.1:2002JAN18	557	576		TM	Transmembrane
85	LG:7696560.1:2002JAN18	577	602		TM	Cytosolic
85	LG:7696560.1:2002JAN18	1135	1194	forward 1	SP	
85	LG:7696560.1:2002JAN18	83	166	forward 2	SP	
86	LG:7698190.26:2002JAN18	1	1466		TM	Extracellular
86	LG:7698190.26:2002JAN18	1467	1489		TM	Transmembrane
86	LG:7698190.26:2002JAN18	1490	1521		TM	Cytosolic
86	LG:7698190.26:2002JAN18	1	1460		TM	Extracellular
86	LG:7698190.26:2002JAN18	1461	1483		TM	Transmembrane
86	LG:7698190.26:2002JAN18	1484	1521		TM	Cytosolic
86	LG:7698190.26:2002JAN18	1	1465		TM	Extracellular
86	LG:7698190.26:2002JAN18	1466	1488		TM	Transmembrane
86	LG:7698190.26:2002JAN18	1489	1520		TM	Cytosolic
86	LG:7698190.26:2002JAN18	2872	2976	forward 1	SP	
86	LG:7698190.26:2002JAN18	4408	4470	forward 1	SP	
87	LG:7763560.12:2002JAN18	1162	1260	forward 1	SP	
87	LG:7763560.12:2002JAN18	2225	2308	forward 2	SP	
87	LG:7763560.12:2002JAN18	2225	2308	forward 2	SP	
88	LG:7763587.20:2002JAN18	431	523	forward 2	SP	
88	LG:7763587.20:2002JAN18	476	520	forward 2	SP	
88	LG:7763587.20:2002JAN18	476	550	forward 2	SP	
88	LG:7763587.20:2002JAN18	1692	1787	forward 3	SP	
89	LG:899263.10:2002JAN18	1	784		TM	Extracellular
89	LG:899263.10:2002JAN18	785	807		TM	Transmembrane
89	LG:899263.10:2002JAN18	808	911		TM	Cytosolic
89	LG:899263.10:2002JAN18	93	167	forward 3	SP	
90	LG:977837.31:2002JAN18	1	55		TM	Extracellular
90	LG:977837.31:2002JAN18	56	78		TM	Transmembrane
90	LG:977837.31:2002JAN18	79	84		TM	Cytosolic
90	LG:977837.31:2002JAN18	85	107		TM	Transmembrane
90	LG:977837.31:2002JAN18	108	320		TM	Extracellular
91	LG:978560.13:2002JAN18	1	1399		TM	Extracellular
91	LG:978560.13:2002JAN18	1400	1419		TM	Transmembrane
91	LG:978560.13:2002JAN18	1420	1426		TM	Cytosolic
91	LG:978560.13:2002JAN18	1	1396		TM	Extracellular
91	LG:978560.13:2002JAN18	1397	1419		TM	Transmembrane
91	LG:978560.13:2002JAN18	1420	1425		TM	Cytosolic
91	LG:978560.13:2002JAN18	2735	2806	forward 2	SP	
91	LG:978560.13:2002JAN18	3971	4039	forward 2	SP	
91	LG:978560.13:2002JAN18	3971	4033	forward 2	SP	
91	LG:978560.13:2002JAN18	2735	2809	forward 2	SP	
91	LG:978560.13:2002JAN18	2735	2806	forward 2	SP	
91	LG:978560.13:2002JAN18	3971	4030	forward 2	SP	



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
91	LG:978560.13:2002JAN18	3971	4033	forward 2	SP	
91	LG:978560.13:2002JAN18	3621	3677	forward 3	SP	
91	LG:978560.13:2002JAN18	3621	3665	forward 3	SP	
91	LG:978560.13:2002JAN18	579	650	forward 3	SP	
91	LG:978560.13:2002JAN18	558	650	forward 3	SP	
91	LG:978560.13:2002JAN18	579	656	forward 3	SP	
91	LG:978560.13:2002JAN18	558	656	forward 3	SP	
91	LG:978560.13:2002JAN18	558	656	forward 3	SP	
92	LG:979390.2:2002JAN18	886	948	forward 1	SP	
92	LG:979390.2:2002JAN18	861	938	forward 3	SP	
92	LG:979390.2:2002JAN18	543	605	forward 3	SP	
92	LG:979390.2:2002JAN18	861	953	forward 3	SP	
92	LG:979390.2:2002JAN18	543	614	forward 3	SP	
93	LG:983019.1:2002JAN18	1338	1397	forward 3	SP	
94	LG:997202.7:2002JAN18	1	1795		TM	Extracellular
94	LG:997202.7:2002JAN18	1796	1818		TM	Transmembrane
94	LG:997202.7:2002JAN18	1819	1837		TM	Cytosolic
94	LG:997202.7:2002JAN18	1838	1860		TM	Transmembrane
94	LG:997202.7:2002JAN18	1861	1869		TM	Extracellular
94	LG:997202.7:2002JAN18	1870	1892		TM	Transmembrane
94	LG:997202.7:2002JAN18	1893	2198		TM	Cytosolic
94	LG:997202.7:2002JAN18	3064	3162	forward 1	SP	
94	LG:997202.7:2002JAN18	3076	3153	forward 1	SP	
94	LG:997202.7:2002JAN18	4567	4626	forward 1	SP	
94	LG:997202.7:2002JAN18	4024	4095	forward 1	SP	
94	LG:997202.7:2002JAN18	3086	3148	forward 2	SP	
94	LG:997202.7:2002JAN18	3086	3157	forward 2	SP	
94	LG:997202.7:2002JAN18	3086	3154	forward 2	SP	
94	LG:997202.7:2002JAN18	3086	3163	forward 2	SP	
94	LG:997202.7:2002JAN18	3086	3163	forward 2	SP	
94	LG:997202.7:2002JAN18	6288	6332	forward 3	SP	
94	LG:997202.7:2002JAN18	738	794	forward 3	SP	
94	LG:997202.7:2002JAN18	6288	6347	forward 3	SP	
94	LG:997202.7:2002JAN18	6288	6347	forward 3	SP	
94	LG:997202.7:2002JAN18	1140	1214	forward 3	SP	
94	LG:997202.7:2002JAN18	1467	1577	forward 3	SP	
94	LG:997202.7:2002JAN18	1134	1214	forward 3	SP	
94	LG:997202.7:2002JAN18	5583	5672	forward 3	SP	
95	LG:998756.3:2002JAN18	1	57		TM	Cytosolic
95	LG:998756.3:2002JAN18	58	77		TM	Transmembrane
95	LG:998756.3:2002JAN18	78	80		TM	Extracellular
95	LG:998756.3:2002JAN18	81	103		TM	Transmembrane
95	LG:998756.3:2002JAN18	104	208		TM	Cytosolic
95	LG:998756.3:2002JAN18	209	231		TM	Transmembrane
95	LG:998756.3:2002JAN18	232	245		TM	Extracellular
95	LG:998756.3:2002JAN18	246	268		TM	Transmembrane
95	LG:998756.3:2002JAN18	269	297		TM	Cytosolic
95	LG:998756.3:2002JAN18	298	320		TM	Transmembrane
95	LG:998756.3:2002JAN18	321	1455		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
95	LG:998756.3:2002JAN18	1	175			
95	LG:998756.3:2002JAN18	176	198		TM	Extracellular
95	LG:998756.3:2002JAN18	199	204		TM	Transmembrane
95	LG:998756.3:2002JAN18	205	224		TM	Cytosolic
95	LG:998756.3:2002JAN18	225	1455		TM	Transmembrane
95	LG:998756.3:2002JAN18	157	234	forward 1	SP	Extracellular
95	LG:998756.3:2002JAN18	157	237	forward 1	SP	
95	LG:998756.3:2002JAN18	157	216	forward 1	SP	
95	LG:998756.3:2002JAN18	157	234	forward 1	SP	
95	LG:998756.3:2002JAN18	716	790	forward 2	SP	
95	LG:998756.3:2002JAN18	716	796	forward 2	SP	
95	LG:998756.3:2002JAN18	716	796	forward 2	SP	
95	LG:998756.3:2002JAN18	716	799	forward 2	SP	
95	LG:998756.3:2002JAN18	1461	1553	forward 3	SP	
95	LG:998756.3:2002JAN18	1461	1559	forward 3	SP	
96	LG:103460.28:2002JAN18	1	88		TM	Cytosolic
96	LG:103460.28:2002JAN18	89	111		TM	Transmembrane
96	LG:103460.28:2002JAN18	112	500		TM	Extracellular
96	LG:103460.28:2002JAN18	501	523		TM	Transmembrane
96	LG:103460.28:2002JAN18	524	663		TM	Cytosolic
96	LG:103460.28:2002JAN18	1	87		TM	Cytosolic
96	LG:103460.28:2002JAN18	88	105		TM	Transmembrane
96	LG:103460.28:2002JAN18	106	662		TM	Extracellular
96	LG:103460.28:2002JAN18	256	324	forward 1	SP	
96	LG:103460.28:2002JAN18	256	339	forward 1	SP	
96	LG:103460.28:2002JAN18	256	330	forward 1	SP	
96	LG:103460.28:2002JAN18	256	330	forward 1	SP	
96	LG:103460.28:2002JAN18	256	324	forward 1	SP	
96	LG:103460.28:2002JAN18	1029	1100	forward 3	SP	
97	LG:1501505.19:2002JAN18	1	48		TM	Cytosolic
97	LG:1501505.19:2002JAN18	49	71		TM	Transmembrane
97	LG:1501505.19:2002JAN18	72	80		TM	Extracellular
97	LG:1501505.19:2002JAN18	81	103		TM	Transmembrane
97	LG:1501505.19:2002JAN18	104	109		TM	Cytosolic
97	LG:1501505.19:2002JAN18	110	132		TM	Transmembrane
97	LG:1501505.19:2002JAN18	133	368		TM	Extracellular
98	LG:233444.9:2002JAN18	1	33		TM	Cytosolic
98	LG:233444.9:2002JAN18	34	56		TM	Transmembrane
98	LG:233444.9:2002JAN18	57	681		TM	Extracellular
98	LG:233444.9:2002JAN18	682	704		TM	Transmembrane
98	LG:233444.9:2002JAN18	705	723		TM	Cytosolic
98	LG:233444.9:2002JAN18	724	746		TM	Transmembrane
98	LG:233444.9:2002JAN18	747	911		TM	Extracellular
98	LG:233444.9:2002JAN18	1	69		TM	Cytosolic
98	LG:233444.9:2002JAN18	70	89		TM	Transmembrane
98	LG:233444.9:2002JAN18	90	103		TM	Extracellular
98	LG:233444.9:2002JAN18	104	126		TM	Transmembrane
98	LG:233444.9:2002JAN18	127	138		TM	Cytosolic
98	LG:233444.9:2002JAN18	139	161		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
98	LG:233444.9:2002JAN18	162	194		TM	Extracellular
98	LG:233444.9:2002JAN18	195	217		TM	Transmembrane
98	LG:233444.9:2002JAN18	218	237		TM	Cytosolic
98	LG:233444.9:2002JAN18	238	260		TM	Transmembrane
98	LG:233444.9:2002JAN18	261	274		TM	Extracellular
98	LG:233444.9:2002JAN18	275	297		TM	Transmembrane
98	LG:233444.9:2002JAN18	298	430		TM	Cytosolic
98	LG:233444.9:2002JAN18	431	453		TM	Transmembrane
98	LG:233444.9:2002JAN18	454	472		TM	Extracellular
98	LG:233444.9:2002JAN18	473	495		TM	Transmembrane
98	LG:233444.9:2002JAN18	496	671		TM	Cytosolic
98	LG:233444.9:2002JAN18	672	694		TM	Transmembrane
98	LG:233444.9:2002JAN18	695	761		TM	Extracellular
98	LG:233444.9:2002JAN18	762	784		TM	Transmembrane
98	LG:233444.9:2002JAN18	785	802		TM	Cytosolic
98	LG:233444.9:2002JAN18	803	825		TM	Transmembrane
98	LG:233444.9:2002JAN18	826	910		TM	Extracellular
98	LG:233444.9:2002JAN18	1	194		TM	Extracellular
98	LG:233444.9:2002JAN18	195	217		TM	Transmembrane
98	LG:233444.9:2002JAN18	218	228		TM	Cytosolic
98	LG:233444.9:2002JAN18	229	251		TM	Transmembrane
98	LG:233444.9:2002JAN18	252	801		TM	Extracellular
98	LG:233444.9:2002JAN18	802	824		TM	Transmembrane
98	LG:233444.9:2002JAN18	825	910		TM	Cytosolic
99	LG:234824.7:2002JAN18	1	1193		TM	Extracellular
99	LG:234824.7:2002JAN18	1194	1216		TM	Transmembrane
99	LG:234824.7:2002JAN18	1217	1227		TM	Cytosolic
99	LG:234824.7:2002JAN18	1228	1250		TM	Transmembrane
99	LG:234824.7:2002JAN18	1251	1253		TM	Extracellular
99	LG:234824.7:2002JAN18	1254	1273		TM	Transmembrane
99	LG:234824.7:2002JAN18	1274	1279		TM	Cytosolic
99	LG:234824.7:2002JAN18	1280	1302		TM	Transmembrane
99	LG:234824.7:2002JAN18	1303	1942		TM	Extracellular
99	LG:234824.7:2002JAN18	1943	1965		TM	Transmembrane
99	LG:234824.7:2002JAN18	1966	1984		TM	Cytosolic
99	LG:234824.7:2002JAN18	1	1945		TM	Extracellular
99	LG:234824.7:2002JAN18	1946	1968		TM	Transmembrane
99	LG:234824.7:2002JAN18	1969	1984		TM	Cytosolic
99	LG:234824.7:2002JAN18	1	1936		TM	Extracellular
99	LG:234824.7:2002JAN18	1937	1956		TM	Transmembrane
99	LG:234824.7:2002JAN18	1957	1984		TM	Cytosolic
99	LG:234824.7:2002JAN18	2337	2408	forward 3	SP	
99	LG:234824.7:2002JAN18	2337	2390	forward 3	SP	
99	LG:234824.7:2002JAN18	2508	2579	forward 3	SP	
99	LG:234824.7:2002JAN18	2721	2822	forward 3	SP	
99	LG:234824.7:2002JAN18	4626	4676	forward 3	SP	
99	LG:234824.7:2002JAN18	2508	2582	forward 3	SP	
100	LG:235708.23:2002JAN18	1	67		TM	Extracellular
100	LG:235708.23:2002JAN18	68	90		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
100	LG:235708.23:2002JAN18	91	101		TM	Cytosolic
100	LG:235708.23:2002JAN18	102	124		TM	Transmembrane
100	LG:235708.23:2002JAN18	125	1270		TM	Extracellular
101	LG:236649.14:2002JAN18	1	457		TM	Extracellular
101	LG:236649.14:2002JAN18	458	480		TM	Transmembrane
101	LG:236649.14:2002JAN18	481	492		TM	Cytosolic
101	LG:236649.14:2002JAN18	493	515		TM	Transmembrane
101	LG:236649.14:2002JAN18	516	529		TM	Extracellular
101	LG:236649.14:2002JAN18	530	552		TM	Transmembrane
101	LG:236649.14:2002JAN18	553	604		TM	Cytosolic
101	LG:236649.14:2002JAN18	1	391		TM	Extracellular
101	LG:236649.14:2002JAN18	392	414		TM	Transmembrane
101	LG:236649.14:2002JAN18	415	455		TM	Cytosolic
101	LG:236649.14:2002JAN18	456	478		TM	Transmembrane
101	LG:236649.14:2002JAN18	479	539		TM	Extracellular
101	LG:236649.14:2002JAN18	540	562		TM	Transmembrane
101	LG:236649.14:2002JAN18	563	603		TM	Cytosolic
101	LG:236649.14:2002JAN18	1	392		TM	Cytosolic
101	LG:236649.14:2002JAN18	393	415		TM	Transmembrane
101	LG:236649.14:2002JAN18	416	454		TM	Extracellular
101	LG:236649.14:2002JAN18	455	477		TM	Transmembrane
101	LG:236649.14:2002JAN18	478	603		TM	Cytosolic
102	LG:332474.7:2002JAN18	1	300		TM	Cytosolic
102	LG:332474.7:2002JAN18	301	320		TM	Transmembrane
102	LG:332474.7:2002JAN18	321	321		TM	Extracellular
102	LG:332474.7:2002JAN18	892	963	forward 1	SP	
102	LG:332474.7:2002JAN18	429	494	forward 3	SP	
102	LG:332474.7:2002JAN18	429	482	forward 3	SP	
102	LG:332474.7:2002JAN18	429	512	forward 3	SP	
102	LG:332474.7:2002JAN18	429	491	forward 3	SP	
102	LG:332474.7:2002JAN18	429	488	forward 3	SP	
103	LG:335727.8:2002JAN18	1	346		TM	Extracellular
103	LG:335727.8:2002JAN18	347	369		TM	Transmembrane
103	LG:335727.8:2002JAN18	370	377		TM	Cytosolic
103	LG:335727.8:2002JAN18	1	214		TM	Extracellular
103	LG:335727.8:2002JAN18	215	237		TM	Transmembrane
103	LG:335727.8:2002JAN18	238	341		TM	Cytosolic
103	LG:335727.8:2002JAN18	342	360		TM	Transmembrane
103	LG:335727.8:2002JAN18	361	377		TM	Extracellular
103	LG:335727.8:2002JAN18	25	90	forward 1	SP	
104	LG:481983.1:2002JAN18	1	19		TM	Extracellular
104	LG:481983.1:2002JAN18	20	42		TM	Transmembrane
104	LG:481983.1:2002JAN18	43	450		TM	Cytosolic
104	LG:481983.1:2002JAN18	451	469		TM	Transmembrane
104	LG:481983.1:2002JAN18	470	488		TM	Extracellular
104	LG:481983.1:2002JAN18	489	511		TM	Transmembrane
104	LG:481983.1:2002JAN18	512	571		TM	Cytosolic
104	LG:481983.1:2002JAN18	572	594		TM	Transmembrane
104	LG:481983.1:2002JAN18	595	603		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
104	LG:481983.1:2002JAN18	604	626		TM	Transmembrane
104	LG:481983.1:2002JAN18	627	928		TM	Cytosolic
104	LG:481983.1:2002JAN18	929	951		TM	Transmembrane
104	LG:481983.1:2002JAN18	952	1382		TM	Extracellular
104	LG:481983.1:2002JAN18	1383	1405		TM	Transmembrane
104	LG:481983.1:2002JAN18	1406	1611		TM	Cytosolic
104	LG:481983.1:2002JAN18	1612	1634		TM	Transmembrane
104	LG:481983.1:2002JAN18	1635	2147		TM	Extracellular
104	LG:481983.1:2002JAN18	2148	2170		TM	Transmembrane
104	LG:481983.1:2002JAN18	2171	2271		TM	Cytosolic
104	LG:481983.1:2002JAN18	1	36		TM	Extracellular
104	LG:481983.1:2002JAN18	37	59		TM	Transmembrane
104	LG:481983.1:2002JAN18	60	159		TM	Cytosolic
104	LG:481983.1:2002JAN18	160	179		TM	Transmembrane
104	LG:481983.1:2002JAN18	180	188		TM	Extracellular
104	LG:481983.1:2002JAN18	189	206		TM	Transmembrane
104	LG:481983.1:2002JAN18	207	243		TM	Cytosolic
104	LG:481983.1:2002JAN18	244	266		TM	Transmembrane
104	LG:481983.1:2002JAN18	267	280		TM	Extracellular
104	LG:481983.1:2002JAN18	281	303		TM	Transmembrane
104	LG:481983.1:2002JAN18	304	447		TM	Cytosolic
104	LG:481983.1:2002JAN18	448	470		TM	Transmembrane
104	LG:481983.1:2002JAN18	471	927		TM	Extracellular
104	LG:481983.1:2002JAN18	928	950		TM	Transmembrane
104	LG:481983.1:2002JAN18	951	969		TM	Cytosolic
104	LG:481983.1:2002JAN18	970	992		TM	Transmembrane
104	LG:481983.1:2002JAN18	993	1160		TM	Extracellular
104	LG:481983.1:2002JAN18	1161	1183		TM	Transmembrane
104	LG:481983.1:2002JAN18	1184	1216		TM	Cytosolic
104	LG:481983.1:2002JAN18	1217	1239		TM	Transmembrane
104	LG:481983.1:2002JAN18	1240	2271		TM	Extracellular
104	LG:481983.1:2002JAN18	1465	1524	forward 1	SP	
104	LG:481983.1:2002JAN18	1465	1518	forward 1	SP	
104	LG:481983.1:2002JAN18	1465	1509	forward 1	SP	
104	LG:481983.1:2002JAN18	3116	3160	forward 2	SP	
104	LG:481983.1:2002JAN18	1271	1345	forward 2	SP	
104	LG:481983.1:2002JAN18	1271	1351	forward 2	SP	
104	LG:481983.1:2002JAN18	570	626	forward 3	SP	
104	LG:481983.1:2002JAN18	831	905	forward 3	SP	
104	LG:481983.1:2002JAN18	1833	1892	forward 3	SP	

TABLE 5

SEQ ID NO./Template ID	Component Span
1/LG:1447398.9:2002JAN18	1513-1947; 1446-1810; 1232-1808; 1394-1805; 1349-1804; 1338-1800; 1394-1800; 1575-1770; 1424-1798; 1540-1780; 1321-1619; 1313-1610; 1232-1482; 993-1458; 1159-1447; 1024-1415; 1174-1389; 998-1286; 601-1232; 836-1212; 724-1168; 905-1163; 706-1161; 798-1161; 909-1161; 914-1161; 927-1161; 777-1161; 746-1160; 739-1153; 646-1100; 662-1100; 627-1100; 693-1100; 715-1100; 628-1100; 663-1100; 563-1082; 492-1077; 888-1066; 717-1062; 635-990; 562-907; 502-903; 580-815; 1-624; 194-484
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5/LG:7685059.6:2002JAN18	1-206; 1-361; 1-263; 36-474; 38-301; 42-307; 63-432; 49-668; 52-363; 52-148; 67-199; 81-662; 76-670; 76-431; 76-320; 76-303; 76-302; 103-368; 110-375; 119-410; 219-386; 218-763; 218-766; 321-560; 440-704
6/LG:7689671.1:2002JAN18	1-451; 1-256; 308-901; 308-557; 308-830; 312-387
7/LG:7689684.1:2002JAN18	1-224; 1-61; 12-96; 111-474; 111-398; 123-518; 123-512; 126-358; 257-609; 305-364
8/LG:7762669.1:2002JAN18	1-255; 1-292; 18-458
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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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36/LG:1502670.1:2002JAN18	1-604; 20-516; 17-163; 21-832; 29-451; 33-286; 37-772; 41-316; 40-294; 43-296; 42-680; 49-787; 49-740; 51-278; 51-108; 57-752; 62-604; 62-310; 63-312; 64-286; 64-369; 66-333; 65-294; 69-340; 70-343; 72-324; 74-780; 72-249; 73-393; 75-348; 77-370; 77-368; 78-376; 80-761; 80-363; 82-369; 81-233; 84-474; 86-426; 85-388; 86-418; 88-390; 87-339; 90-685; 90-350; 92-391; 94-801; 94-387; 95-374; 100-368; 97-578; 107-223; 106-368; 194-584; 207-296; 286-515; 287-461; 295-358; 472-782; 538-745; 538-782; 675-782; 712-782
37/LG:206593.3:2002JAN18	1-537; 13-376; 16-229; 310-770; 451-538; 451-649; 456-652; 486-650; 550-868; 567-731; 606-757; 601-1290; 644-1311; 643-1108; 722-1290; 816-1403; 879-1410; 879-1139; 882-1179; 934-1328; 911-1140; 945-1211; 946-1448; 1004-1549; 1075-1256; 1101-1519; 1138-1266; 1148-1549

TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

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TABLE 5

SEQ ID NO: / Template ID	Component Span
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101/LG:236649.14:2002JAN18	1-501; 203-366; 283-868; 304-914; 326-632; 326-591; 340-813; 342-603; 365-539; 380-598; 400-632; 412-863; 412-654; 416-995; 416-707; 421-617; 425-591; 475-587; 475-591; 518-795; 522-790; 525-806; 548-803; 551-793; 564-825; 597-917; 594-841; 603-812; 615-1168; 615-890; 656-962; 662-1167; 662-931; 671-1250; 677-979; 680-968; 682-991; 686-940; 696-1012; 708-1168; 715-945; 714-957; 721-1009; 726-958; 726-1161; 751-1012; 782-1021; 784-997; 785-1033; 785-1062; 800-1060; 820-1302; 832-1079; 852-1112; 868-985; 888-1104; 891-1358; 905-1352; 906-1347; 925-1314; 929-1207; 945-1192; 951-1527; 961-1202; 976-1360; 985-1201; 998-1180; 998-1193; 1000-1222; 1009-1358; 1011-1358; 1018-1490; 1043-1306; 1046-1354; 1051-1328; 1052-1352; 1061-1229; 1085-1530; 1098-1208; 1120-1392; 1147-1521; 1147-1513; 1164-1525; 1166-1382; 1220-1491; 1234-1504; 1372-1624; 1372-1603; 1471-1810; 1501-1756; 1501-1739; 1579-1803; 1594-1812
102/LG:332474.7:2002JAN18	1-261; 1-398; 5-654; 153-437; 333-805; 338-744; 356-910; 396-944; 396-649; 614-805; 646-968; 820-958; 824-963
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TABLE 5

SEQ ID NO./Template ID	Component Span
104/LG:481983.1:2002JAN18	1-615; 1-645; 1-644; 73-645; 571-930; 571-805; 642-905; 645-843; 677-1021; 797-1071; 797-1069; 824-1028; 860-1167; 909-1510; 970-1225; 972-1380; 987-1559; 1005-1622; 1066- 1581; 1069-1614; 1077-1623; 1117-1527; 1117-1260; 1139-1551; 1152-1577; 1181-1357; 1194- 1382; 1229-1687; 1268-1542; 1291-1723; 1293-1722; 1303-1709; 1312-1747; 1322-1691; 1356- 1730; 1392-1655; 1394-1595; 1411-1585; 1411-1724; 1411-1683; 1411-1681; 1418-1688; 1510- 1724; 1552-1672; 1587-1719; 1609-1849; 1640-1845; 1652-2103; 1760-1973; 1785-2230; 1902- 2226; 2060-2682; 2100-2581; 2322-2821; 2469-2776; 2479-3028; 2598-3092; 2639-2925; 2708- 3251; 3026-3300; 3043-3799; 3072-3342; 3113-3669; 3186-3434; 3399-3547; 3415-3630; 3416- 3658; 3421-3815; 3440-3686; 3441-3919; 3455-3919; 3468-3787; 3478-3743; 3502-3786; 3563- 3801; 3563-4115; 3632-4139; 3632-3825; 3632-3892; 3676-4183; 3651-3888; 3676-4126; 3680- 3991; 3684-3951; 3695-3807; 3747-4143; 3749-4260; 3801-4255; 3801-4012; 3833-3994; 3861- 4142; 3900-4238; 3905-4107; 3910-4521; 3912-4156; 3951-4414; 3994-4256; 4032-4606; 4040- 4813; 4079-4423; 4115-4405; 4124-4265; 4128-4727; 4184-4458; 4197-4639; 4200-4567; 4200-4469; 4207-4608; 4217-4378; 4279-4810; 4309-4604; 4312-4768; 4321-4484; 4317-4931; 4335-4610; 4339-4861; 4344-4932; 4342-4626; 4387-4643; 4387-4614; 4404-4650; 4423-4674; 4443-4701; 4492-4768; 4523-4939; 4530-4765; 4558-5171; 4560-4821; 4567-4854; 4577-4692; 4588-4813; 4588-4881; 4597-4839; 4605-5037; 4604-5109; 4646-4966; 4646-4890; 4697-5418; 4705-4919; 4734-5000; 4778-5092; 4797-5098; 4823-5063; 4823-4946; 4860-5161; 4868-5065; 4869-5427; 4871-5332; 4872-5111; 4887-5501; 4898-5126; 4898-5122; 4898-5111; 4898-5129; 4901-5163; 4939-5240; 4943-5166; 4951-5619; 4959-5438; 4973-5262; 4974-5239; 5032-5301; 5035-5373; 5059-5163; 5062-5652; 5088-5752; 5083-5453; 5083-5241; 5083-5515; 5091-5710; 5110-5488; 5110-5361; 5113-5295; 5125-5286; 5128-5426; 5138-5390; 5153-5465; 5156-5435; 5157-5406; 5163-5749; 5194-5410; 5223-6011; 5213-5429; 5253-5819; 5259-5488; 5294-5541; 5296-5919; 5312-5774; 5312-5846; 5312-5808; 5312-5912; 5315-5844; 5328-5757; 5339-5416; 5341-5881; 5376-5553; 5388-6147; 5428-5688; 5440-5670; 5431-5896; 5444-5720; 5436-5701; 5439-5554; 5459-5719; 5463-5730; 5492-5718; 5497-5752; 5488-5880; 5493-5708; 5492-5734;



TABLE 5

SEQ ID NO./Template ID	Component Span
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TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
1	LG:1447398.9:2002JAN18	Germ Cells - 42%, Skin - 28%
2	LG:201488.3:2002JAN18	Female Genitalia - 13%, Cardiovascular System - 12%, Unclassified/Mixed - 11%
3	LG:288410.6:2002JAN18	Urinary Tract - 33%, Male Genitalia - 22%, Endocrine System - 22%
4	LG:7682817.1:2002JAN18	Cardiovascular System - 33%, Hemic and Immune System - 25%, Exocrine Glands - 25%
5	LG:7685059.6:2002JAN18	Liver - 27%, Skin - 23%, Hemic and Immune System - 15%, Endocrine System - 15%
6	LG:7689671.1:2002JAN18	Digestive System - 75%, Nervous System - 25%
7	LG:7689684.1:2002JAN18	Digestive System - 30%, Hemic and Immune System - 30%, Male Genitalia - 20%, Female Genitalia - 18%
8	LG:7762669.1:2002JAN18	Pancreas - 82%, Digestive System - 18%
9	LG:965822.1:2002JAN18	Skin - 43%, Sense Organs - 29%, Germ Cells - 19%
10	LG:006394.31:2002JAN18	Sense Organs - 15%, Digestive System - 14%, Germ Cells - 13%
11	LG:018258.1:2002JAN18	Urinary Tract - 43%, Endocrine System - 29%, Digestive System - 21%
12	LG:027320.5:2002JAN18	Germ Cells - 33%, Embryonic Structures - 18%
13	LG:057499.1:2002JAN18	Skin - 13%
14	LG:065935.21:2002JAN18	Stomatognathic System - 30%, Unclassified/Mixed - 13%
15	LG:071860.12:2002JAN18	Exocrine Glands - 35%, Unclassified/Mixed - 25%, Endocrine System - 20%
16	LG:087383.29:2002JAN18	Sense Organs - 24%, Embryonic Structures - 16%
17	LG:098580.3:2002JAN18	Unclassified/Mixed - 38%, Cardiovascular System - 31%, Endocrine System - 31%
18	LG:1001879.1:2002JAN18	Unclassified/Mixed - 38%, Hemic and Immune System - 23%, Nervous System - 23%
19	LG:1079456.4:2002JAN18	Liver - 35%, Musculoskeletal System - 30%, Endocrine System - 20%
20	LG:1080598.9:2002JAN18	Germ Cells - 21%, Embryonic Structures - 15%
21	LG:1090358.10:2002JAN18	Liver - 25%, Embryonic Structures - 18%, Pancreas - 11%
22	LG:1097492.2:2002JAN18	Urinary Tract - 10%
23	LG:1099945.26:2002JAN18	Musculoskeletal System - 13%, Germ Cells - 11%
24	LG:110016.1:2002JAN18	Musculoskeletal System - 53%, Embryonic Structures - 12%
25	LG:1137613.10:2002JAN18	widely distributed
26	LG:118836.26:2002JAN18	Endocrine System - 13%, Connective Tissue - 12%, Hemic and Immune System - 10%
27	LG:1330261.32:2002JAN18	Male Genitalia - 17%, Cardiovascular System - 14%, Female Genitalia - 13%
28	LG:1347461.28:2002JAN18	Unclassified/Mixed - 29%, Hemic and Immune System - 11%
29	LG:1383494.16:2002JAN18	Sense Organs - 12%, Liver - 11%
30	LG:1400155.1:2002JAN18	Urinary Tract - 14%, Unclassified/Mixed - 10%
31	LG:1446621.1:2002JAN18	Endocrine System - 63%, Urinary Tract - 16%, Female Genitalia - 11%, Nervous System - 11%
32	LG:144920.1:2002JAN18	Liver - 23%, Unclassified/Mixed - 17%, Respiratory System - 15%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
33	LG:1452619.1:2002JAN18	widely distributed
34	LG:1453417.6:2002JAN18	Nervous System - 26%, Skin - 16%, Female Genitalia - 13%
35	LG:148485.8:2002JAN18	Sense Organs - 16%
36	LG:1502670.1:2002JAN18	Cardiovascular System - 15%, Endocrine System - 12%
37	LG:206593.3:2002JAN18	Exocrine Glands - 25%, Unclassified/Mixed - 18%, Nervous System - 14%, Endocrine System - 14%
38	LG:228273.22:2002JAN18	Nervous System - 16%, Unclassified/Mixed - 15%, Embryonic Structures - 11%
39	LG:228319.2:2002JAN18	Musculoskeletal System - 33%, Male Genitalia - 22%, Hemic and Immune System - 22%
40	LG:229165.16:2002JAN18	Unclassified/Mixed - 28%, Skin - 21%, Exocrine Glands - 11%
41	LG:230895.9:2002JAN18	Unclassified/Mixed - 40%, Respiratory System - 20%, Nervous System - 20%
42	LG:233552.5:2002JAN18	Germ Cells - 18%
43	LG:234430.7:2002JAN18	Sense Organs - 19%, Nervous System - 19%
44	LG:236659.1:2002JAN18	Unclassified/Mixed - 12%
45	LG:236767.26:2002JAN18	Musculoskeletal System - 18%, Sense Organs - 16%
46	LG:237489.7:2002JAN18	Pancreas - 36%, Respiratory System - 23%, Urinary Tract - 12%, Skin - 12%
47	LG:238218.20:2002JAN18	Liver - 10%
48	LG:239939.14:2002JAN18	Germ Cells - 32%, Connective Tissue - 11%, Nervous System - 11%
49	LG:242288.11:2002JAN18	Pancreas - 12%
50	LG:242491.29:2002JAN18	Sense Organs - 24%, Digestive System - 12%, Liver - 10%
51	LG:243488.41:2002JAN18	Male Genitalia - 17%, Endocrine System - 11%
52	LG:247792.18:2002JAN18	Sense Organs - 24%
53	LG:253193.17:2002JAN18	Pancreas - 39%, Hemic and Immune System - 24%, Embryonic Structures - 11%
54	LG:257088.20:2002JAN18	Unclassified/Mixed - 14%, Digestive System - 11%
55	LG:265552.1:2002JAN18	Sense Organs - 48%, Digestive System - 31%, Exocrine Glands - 10%
56	LG:275355.12:2002JAN18	Musculoskeletal System - 20%, Exocrine Glands - 18%, Female Genitalia - 14%
57	LG:280014.1:2002JAN18	Skin - 55%, Musculoskeletal System - 27%, Digestive System - 14%
58	LG:299937.3:2002JAN18	Stomatognathic System - 14%, Embryonic Structures - 11%
59	LG:311197.3:2002JAN18	Skin - 30%, Digestive System - 17%, Pancreas - 12%
60	LG:321069.2:2002JAN18	Stomatognathic System - 14%, Germ Cells - 13%, Urinary Tract - 12%
61	LG:330900.8:2002JAN18	Germ Cells - 16%, Hemic and Immune System - 11%
62	LG:330931.9:2002JAN18	Unclassified/Mixed - 12%, Embryonic Structures - 12%, Male Genitalia - 11%
63	LG:330985.1:2002JAN18	Germ Cells - 21%, Unclassified/Mixed - 15%
64	LG:332027.9:2002JAN18	Sense Organs - 21%, Liver - 13%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
65	LG:335377.8:2002JAN18	Unclassified/Mixed - 24%, Nervous System - 22%, Male Genitalia - 19%
66	LG:337452.25:2002JAN18	Germ Cells - 36%, Male Genitalia - 12%
67	LG:340580.16:2002JAN18	Female Genitalia - 11%
68	LG:350272.6:2002JAN18	Embryonic Structures - 13%, Musculoskeletal System - 12%
69	LG:397228.1:2002JAN18	Unclassified/Mixed - 42%, Cardiovascular System - 33%, Male Genitalia - 17%
70	LG:401325.41:2002JAN18	Nervous System - 19%, Skin - 12%, Unclassified/Mixed - 10%
71	LG:402029.14:2002JAN18	Respiratory System - 17%, Male Genitalia - 15%, Digestive System - 13%
72	LG:407233.2:2002JAN18	Endocrine System - 28%, Hemic and Immune System - 24%, Skin - 21%
73	LG:407346.1:2002JAN18	Sense Organs - 29%, Nervous System - 26%, Hemic and Immune System - 11%
74	LG:407689.7:2002JAN18	Digestive System - 14%, Nervous System - 11%, Hemic and Immune System - 11%
75	LG:407700.1:2002JAN18	Skin - 21%, Digestive System - 10%
76	LG:410461.92:2002JAN18	Musculoskeletal System - 19%, Liver - 19%, Endocrine System - 18%
77	LG:411043.3:2002JAN18	Pancreas - 16%, Exocrine Glands - 12%, Nervous System - 12%
78	LG:438690.47:2002JAN18	widely distributed
79	LG:444677.81:2002JAN18	Sense Organs - 31%, Urinary Tract - 15%, Skin - 12%, Male Genitalia - 12%
80	LG:457464.24:2002JAN18	Skin - 13%, Hemic and Immune System - 10%
81	LG:7684793.15:2002JAN18	Skin - 15%, Germ Cells - 10%
82	LG:7687485.1:2002JAN18	Cardiovascular System - 26%, Musculoskeletal System - 26%, Urinary Tract - 14%
83	LG:7689661.4:2002JAN18	Musculoskeletal System - 28%, Urinary Tract - 11%, Nervous System - 10%, Endocrine System - 10%
84	LG:7690373.1:2002JAN18	Male Genitalia - 40%, Nervous System - 40%, Hemic and Immune System - 20%
85	LG:7696560.1:2002JAN18	Nervous System - 53%, Pancreas - 47%
86	LG:7698190.26:2002JAN18	widely distributed
87	LG:7763560.12:2002JAN18	Sense Organs - 10%
88	LG:7763587.20:2002JAN18	Sense Organs - 23%, Musculoskeletal System - 12%
89	LG:899263.10:2002JAN18	Female Genitalia - 16%, Nervous System - 16%, Embryonic Structures - 14%, Exocrine Glands - 14%, Liver - 14%
90	LG:977837.31:2002JAN18	Liver - 41%, Respiratory System - 29%, Unclassified/Mixed - 29%
91	LG:978560.13:2002JAN18	Germ Cells - 11%, Embryonic Structures - 11%
92	LG:979390.2:2002JAN18	Pancreas - 25%, Connective Tissue - 19%, Liver - 19%
93	LG:983019.1:2002JAN18	Embryonic Structures - 37%, Germ Cells - 29%, Unclassified/Mixed - 11%
94	LG:997202.7:2002JAN18	Skin - 11%, Exocrine Glands - 10%
95	LG:998756.3:2002JAN18	Germ Cells - 20%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
96	LG:103460.28:2002JAN18	Germ Cells - 10%
97	LG:1501505.19:2002JAN18	Musculoskeletal System - 50%, Male Genitalia - 33%, Digestive System - 17%
98	LG:233444.9:2002JAN18	Sense Organs - 14%, Urinary Tract - 12%
99	LG:234824.7:2002JAN18	Germ Cells - 21%, Sense Organs - 18%
100	LG:235708.23:2002JAN18	Digestive System - 25%, Liver - 22%, Male Genitalia - 16%
101	LG:236649.14:2002JAN18	Germ Cells - 15%, Musculoskeletal System - 10%
102	LG:332474.7:2002JAN18	Urinary Tract - 56%, Nervous System - 25%, Female Genitalia - 13%
103	LG:335727.8:2002JAN18	Endocrine System - 19%, Cardiovascular System - 18%, Musculoskeletal System - 18%
104	LG:481983.1:2002JAN18	Germ Cells - 12%

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
105	2	168	536	1039	g2827474	1.00E-89	predicted protein dJ257A7.2
105	2	168	536	1039	g15485622	2.00E-51	Q9H4T4 like
105	2	168	536	1039	g10241527	2.00E-51	dJ899C14.1 (novel protein similar to KIAA0680)
106	3	224	3	674	g6599307	1.00E-98	LIM domains containing protein 1
106	3	224	3	674	g12836264	2.00E-98	LIM domains containing 1~data source:MGD, source key:MGI:1352502, evidence:ISS~putative
106	3	224	3	674	g6599070	2.00E-96	LIM domains containing protein 1
107	2	173	614	1132	g24416557	1.00E-87	Similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7
107	2	173	614	1132	g15823642	1.00E-87	ALS2CR7
107	2	173	614	1132	g4240157	6.00E-51	KIAA0834 protein
108	3	168	870	1373	g20072170	3.00E-20	Unknown (protein for MGC:27348)
108	3	168	870	1373	g2231145	2.00E-15	putative
108	3	168	870	1373	g6522712	1.00E-08	dJ688G8.1 (Similar to ribosomal protein S2 (RPS2) )
109	2	187	206	766	g21750807	7.00E-91	unnamed protein product
109	2	187	206	766	g10439850	4.00E-31	unnamed protein product
109	2	187	206	766	g18916783	2.00E-23	KIAA1956 protein
110	2	73	452	670	g930123	4.00E-10	zinc finger protein (583 AA)
110	2	73	452	670	g21758286	5.00E-10	unnamed protein product
110	2	73	452	670	g22760554	8.00E-10	unnamed protein product
111	2	182	59	604	g21739498	2.00E-77	hypothetical protein
111	2	182	59	604	g23273014	2.00E-76	hypothetical protein FLJ37933
111	2	182	59	604	g21754469	4.00E-76	unnamed protein product
111	2	182	59	604	g21754722	2.00E-22	unnamed protein product
112	1	108	133	456	g15080547	2.00E-17	Unknown (protein for MGC:21259)
112	1	108	133	456	g1049301	2.00E-17	KRAB zinc finger protein; Method: conceptual translation supplied by
112	1	108	133	456	g22760908	2.00E-40	unnamed protein product
113	1	240	1	720	g13623633	5.00E-18	Unknown (protein for MGC:13105)
113	1	240	1	720	g16551840	8.00E-16	unnamed protein product
113	1	240	1	720	g6808105	1.00E-79	hypothetical protein
114	2	319	1367	2323	g21739797	2.00E-79	hypothetical protein
114	2	319	1367	2323	g19353175	3.00E-79	Unknown (protein for MGC:28436)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability	Score	Annotation
115	2	263	2	790	g19483967	1.00E-110		RIKEN cDNA 061009A07 gene
115	2	263	2	790	g12832288	1.00E-110		data source:SPTR, source key:O75989, evidence:ISS-homolog to ELEGANS DJ422F24.1 (PUTATIVE NOVEL PROTEIN SIMILAR TO C. ELEGANS C02C2.5) (FRAGMENT)-putative
115	2	263	2	790	g3757719	2.00E-87		dj422f24.1 (PUTATIVE novel protein similar to C. elegans C02C2.5)
116	3	449	3	1349	g12839186	0.00		data source:SPTR, source key:Q9VS60, evidence:ISS-putative-related to CG8576 PROTEIN
116	3	449	3	1349	g16553765	0.00		unnamed protein product
116	3	449	3	1349	g23094020	1.00E-108		CG32380-PA
117	1	601	1	1803	g5689563	0.00		KIAA1113 protein
117	1	601	1	1803	g12407441	0.00		tripartite motif protein TRIM33 alpha
117	1	601	1	1803	g5834582	0.00		rfg7 protein
118	2	170	17	526	g16041781	6.00E-85		Similar to RIKEN cDNA 0710001C05 gene
118	2	170	17	526	g23273089	4.00E-82		Unknown (protein for MGC:43081)
118	2	170	17	526	g12833285	3.00E-65		HesB-like domain containing protein~data source: Pfam, source key:PF01521, evidence:ISS-putative
119	3	106	456	773	g9294743	8.00E-37		MAGOH isoform
119	3	106	456	773	g7022229	8.00E-37		unnamed protein product
119	3	106	456	773	g4894380	8.00E-37		Mago homolog
120	2	334	95	1096	g14165480	1.00E-178		Unknown (protein for MGC:1214)
120	2	334	95	1096	g12053195	1.00E-178		hypothetical protein
120	2	334	95	1096	g5305706	1.00E-177		cytoplasmic phosphoprotein PACSIN2
121	2	109	11	337	g17381941	2.00E-43		unnamed protein product
121	2	109	11	337	g999454	7.00E-30		TX protease precursor
121	2	109	11	337	g903934	7.00E-30		cysteine protease
122	1	519	1	1557	g23342615	0.00		unnamed protein product
122	1	519	1	1557	g21899842	0.00		unnamed protein product
122	1	519	1	1557	g21886479	0.00		unnamed protein product
123	3	132	3	398	g21336362	3.00E-24		unnamed protein product
123	3	132	3	398	g21757193	5.00E-22		unnamed protein product
123	3	132	3	398	g7023216	4.00E-17		unnamed protein product
124	2	524	290	1861	g21618499	0.00		Similar to hypothetical protein FLJ20079

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
124	2	524	290	1861	g7019945	1.00E-179	unnamed protein product
124	2	524	290	1861	g22760462	1.00E-165	unnamed protein product
125	1	309	685	1611	g3540177	1.00E-109	F23269_2
125	1	309	685	1611	g5080758	1.00E-108	BC331191_1
125	1	309	685	1611	g12855931	5.00E-63	data source:SPTR, source key:P16374, evidence:ISS-putative~similar to ZINC FINGER PROTEIN 60 (ZFP-60) (ZINC FINGER PROTEIN MFG-3)
126	2	339	1979	2995	g10047329	1.00E-178	KIAA1626 protein
126	2	339	1979	2995	g18256873	1.00E-161	Unknown (protein for IMAGE:4016433)
126	2	339	1979	2995	g7022610	1.00E-151	unnamed protein product
127	2	163	2	490	g12842823	2.00E-38	data source:SPTR, source key:P02403, evidence:ISS-homolog to 60S RIBOSOMAL PROTEIN L37 (G1.16)-putative
127	2	163	2	490	g57121	4.00E-38	ribosomal protein L37
127	2	163	2	490	g461232	4.00E-38	ribosomal protein L37
128	1	352	259	1314	g16552019	1.00E-109	unnamed protein product
128	1	352	259	1314	g12844321	1.00E-96	data source:SPTR, source key:Q9ER30, evidence:ISS-homolog to KELCH-RELATED PROTEIN 1 (KEL-LIKE PROTEIN 23) (SARCOSIN)-putative
128	1	352	259	1314	g16306813	8.00E-39	Unknown (protein for MGC:1367)
129	2	138	2	415	g7582193	5.00E-22	dynein light chain 1 protein DLC-1
129	2	138	2	415	g470344	5.00E-22	C. elegans DLC-1 protein (corresponding sequence T26A5.9)
129	2	138	2	415	g4103059	5.00E-22	protein inhibitor of nitric oxide synthase
130	2	608	1148	2971	g7959175	0.00	KIAA1457 protein
130	2	608	1148	2971	g6599224	0.00	hypothetical protein
130	2	608	1148	2971	g12667438	0.00	NIR3
131	1	694	460	2541	g4929551	0.00	CGI-40 protein
131	1	694	460	2541	g23274030	0.00	Similar to CGI-40 protein
131	1	694	460	2541	g22761032	0.00	unnamed protein product
132	3	401	231	1433	g23242933	0.00	Unknown (protein for MGC:46349)
132	3	401	231	1433	g21755437	0.00	unnamed protein product
132	3	401	231	1433	g20515159	3.00E-15	conserved hypothetical protein
133	3	141	474	896	g4929669	2.00E-70	CGI-100 protein
133	3	141	474	896	g16741027	2.00E-70	CGI-100 protein
133	3	141	474	896	g11596068	2.00E-70	dJ976O13.1 (CGI-100 protein)



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
134	2	340	392	1411	g4164365	0.00	dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24))
134	2	340	392	1411	g3766467	0.00	NAD+ dependent succinic semialdehyde dehydrogenase
134	2	340	392	1411	g21708023	0.00	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)
135	3	229	312	998	g7959207	3.00E-38	KIAA1473 protein
135	3	229	312	998	g21265141	7.00E-36	Similar to zinc finger protein 91 (HPF7, HTF10)
135	3	229	312	998	g3342002	9.00E-36	hematopoietic cell derived zinc finger protein
136	1	407	1	1221	g2689444	1.00E-141	ZNF134
136	1	407	1	1221	g10440218	1.00E-130	unnamed protein product
136	1	407	1	1221	g16553223	1.00E-128	unnamed protein product
137	2	529	2	1588	g22477301	0.00	Unknown (protein for MGC:46140)
137	2	529	2	1588	g12852385	0.00	CUG triplet repeat, RNA binding protein 1~data source:MGD, source key:MG1:1342295, evidence:ISS~putative
137							RNA-binding protein BRUNO12
137	2	529	2	1588	g9246973	0.00	FLAMINGO 1
138	1	2245	2254	8988	g9828190	0.00	seven transmembrane helix receptor
138	1	2245	2254	8988	g21929188	0.00	Similar to D.melanogaster cadherin-related tumor suppressor
138	1	2245	2254	8988	g1665821	0.00	Unknown (protein for MGC:40579)
139	1	490	1	1470	g21595468	1.00E-159	unnamed protein product
139	1	490	1	1470	g21749150	1.00E-116	CG1271-PA
139	1	490	1	1470	g23095363	6.00E-97	data source:SPTR, source key:P41276, evidence:ISS~homolog to ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 1~putative
140	2	190	2	571	g12843886	1.00E-15	putative
140	2	190	2	571	g607028	2.00E-15	ADP-ribosylation factor-like protein 1
140	2	190	2	571	g20147667	2.00E-15	Zinc finger protein s11-6
141	2	153	692	1150	g3953593	2.00E-51	Unknown (protein for MGC:25259)
141	2	153	692	1150	g15928468	2.00E-51	unnamed protein product
141	2	153	692	1150	g21751975	3.00E-51	KIAA0681 protein
142	1	608	583	2406	g3327176	0.00	dJ138B7.3.2 (lethal (3) malignant brain tumor ((3)mbt) protein (Drosophila) homolog (isoform 2) (KIAA0681))
142	1	608	583	2406	g11323324	0.00	((3)mbt protein homolog
142	1	608	583	2406	g3811111	0.00	

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
143	1	265	646	1440	g21752073	1.00E-148	unnamed protein product
143	1	265	646	1440	g16041142	1.00E-133	hypothetical protein
143	1	265	646	1440	g14017813	1.00E-88	KIAA1798 protein
144	2	687	8	2068	g12024744	0.00	TA p63 alpha
144	2	687	8	2068	g3970717	0.00	KET protein
144	2	687	8	2068	g3695094	0.00	TA* p63 alpha
145	1	478	1	1434	g15620895	0.00	KIAA1918 protein
145	1	478	1	1434	g971459	0.00	UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
145	1	478	1	1434	g304259	0.00	UDP-GalNAc:polypeptide, N-acetylgalactosaminyl transferase
146	1	946	274	3111	g10047283	0.00	KIAA1604 protein
146	1	946	274	3111	g10439972	0.00	unnamed protein product
146	1	946	274	3111	g10438214	0.00	unnamed protein product
147	3	318	3	956	g6572215	1.00E-170	dJ37E16.5 (novel protein similar to nitrophenylphosphatases from various organisms)
147	3	318	3	956	g12653107	1.00E-170	hypothetical protein dJ37E16.5
147	3	318	3	956	g14602499	5.00E-99	Similar to hypothetical protein dJ37E16.5
148	3	1632	3	4898	g12083896	0.00	polybromo-1
148	3	1632	3	4898	g12083875	0.00	polybromo-1
148	3	1632	3	4898	g16607752	0.00	unnamed protein product
149	2	736	2	2209	g12836469	0.00	data source:SPTR, source key:Q9HCJ3, evidence:ISS-homolog to KIAA1579
149	2	736	2	2209	g22902182	0.00	PROTEIN (FRAGMENT)-putative
149	2	736	2	2209	g22766819	0.00	Unknown (protein for IMAGE:5113697)
150	1	323	157	1125	g16588681	1.00E-161	Unknown (protein for MGC:46327)
150	1	323	157	1125	g15341556	1.00E-161	anion transporter/exchanger-9
150	1	323	157	1125	g14787223	2.00E-29	putative anion transporter
151	1	628	1	1884	g7959287	0.00	prestin
151	1	628	1	1884	g20146520	1.00E-101	KIAA1513 protein
151	1	628	1	1884	g14670188	3.00E-27	SLTP003
152	3	183	324	872	g21758740	3.00E-92	Hypothetical protein W02H5.4
152	3	183	324	872	g20073240	3.00E-92	unnamed protein product
152	3	183	324	872	g15795887	3.00E-92	similar to putative
							unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
153	1	338	499	1512	g6329959	1.00E-132	KIAA1142 protein
153	1	338	499	1512	g4164385	1.00E-132	PAK4 protein
153	1	338	499	1512	g4101587	1.00E-132	serine/threonine kinase
154	1	191	25	597	g22760075	1.00E-103	unnamed protein product
154	1	191	25	597	g15209772	3.00E-99	unnamed protein product
154	1	191	25	597	g20377682	5.00E-92	P26 protein
155	3	317	3	953	g21542541	1.00E-119	Similar to HTPAP protein
155	3	317	3	953	g13182757	3.00E-85	HTPAP
155	3	317	3	953	g12844263	3.00E-58	data source:SPTR, source key:Q9VND5, evidence:ISS-putative~related to CG12746 PROTEIN
156	2	617	8	1858	g23273603	0.00	Unknown (protein for MGC:37640)
156	2	617	8	1858	g10041649	0.00	unnamed protein product
156	2	617	8	1858	g23271317	0.00	Unknown (protein for MGC:33943)
157	3	371	1197	2309	g20988140	0.00	E74-like factor 1 (ets domain transcription factor)
157	3	371	1197	2309	g15010800	0.00	Ets-family transcription factor ELF1
157	3	371	1197	2309	g11995007	0.00	transcription factor Elf-1
158	2	871	989	3601	g20372683	0.00	euchromatic histone methyltransferase 1
158	2	871	989	3601	g10434623	0.00	unnamed protein product
158	2	871	989	3601	g20522002	0.00	KIAA1876 protein
159	2	157	152	622	g18490501	1.00E-56	RIKEN cDNA 201002A20 gene
159	2	157	152	622	g12843712	1.00E-56	Immunoglobulin domain containing protein~data source: Pfam, source key:PF00047, evidence:ISS-putative
159	2	157	152	622	g12841961	1.00E-50	Immunoglobulin domain containing protein~data source: Pfam, source key:PF00047, evidence:ISS-putative
160	1	280	10	849	g23451450	1.00E-122	ATP-binding cassette sub-family A member 9
160	1	280	10	849	g23451407	1.00E-122	ATP-binding cassette sub-family A member 9
160	1	280	10	849	g17223624	1.00E-121	ATP-binding cassette A9
161	1	149	559	1005	g18088580	1.00E-80	Unknown (protein for MGC:23949)
161	1	149	559	1005	g12860781	1.00E-30	claudin 14~data source:MGD, source key:MG1:1860425, evidence:ISS-putative
161	1	149	559	1005	g13452508	1.00E-30	claudin 14
162	3	281	270	1112	g16549414	1.00E-155	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
162	3	281	270	1112	g13938457	1.00E-155	Unknown (protein for MGC:16175)
162	3	281	270	1112	g13436338	1.00E-77	Unknown (protein for IMAGE:3625550)
163	3	703	312	2420	g13811938	0.00	dJ1056H1.2.1 (novel protein similar to mitogen Inducible protein MIG-2 (isoform 1))
163	3	703	312	2420	g23273527	0.00	Unknown (protein for MGC:46404)
163	3	703	312	2420	g16878257	0.00	Unknown (protein for MGC:29726)
164	1	128	439	822	g24059753	5.00E-64	hypothetical protein
164	1	128	439	822	g12856090	9.00E-62	data source:SPTR, source key:Q9Z2B2, evidence:ISS-putative~similar to BRAIN MITOCHONDRIAL CARRIER PROTEIN-1 (BMCP-1)
164	1	128	439	822	g12854104	9.00E-62	data source:SPTR, source key:Q9Z2B2, evidence:ISS-putative~similar to BRAIN MITOCHONDRIAL CARRIER PROTEIN-1 (BMCP-1)
165	2	1250	2	3751	g21756799	0.00	unnamed protein product
165	2	1250	2	3751	g13938013	0.00	Similar to RIKEN cDNA 2610509G12 gene
165	2	1250	2	3751	g6650822	0.00	PRO2000
166	1	705	1	2115	g13365895	0.00	hypothetical protein
166	1	705	1	2115	g21749428	0.00	unnamed protein product
166	1	705	1	2115	g1842216	8.00E-17	Zfp64
167	3	630	3	1892	g717056	0.00	reduced folate carrier protein
167	3	630	3	1892	g2209135	0.00	folate carrier
167	3	630	3	1892	g2967654	0.00	reduced folate carrier
168	3	389	132	1298	g12832845	1.00E-161	Domain of unknown function DUF36 containing protein~data source:Pfam, source key:PF01795, evidence:ISS-putative
168	3	389	132	1298	g21749636	1.00E-136	unnamed protein product
168	3	389	132	1298	g21410962	1.00E-70	Unknown (protein for MGC:32708)
169	2	381	83	1225	g5114351	1.00E-165	RING finger protein ferf
169	2	381	83	1225	g21707131	1.00E-165	tripartite motif-containing 17
169	2	381	83	1225	g5114353	1.00E-118	RING finger protein ferf
170	3	659	3	1979	g14017797	0.00	KIAA1790 protein
170	3	659	3	1979	g13529311	1.00E-126	Similar to hypothetical protein FLJ23119
170	3	659	3	1979	g10439701	1.00E-109	unnamed protein product
171	2	219	1253	1909	g8096557	1.00E-84	PBX1B
171	2	219	1253	1909	g8096555	1.00E-84	PBX1A

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
171	2	219	1253	1909	g456109	1.00E-84	homeobox protein
172	2	438	2	1315	g22859174	0.00	hypothetical protein
172	2	438	2	1315	g12845866	1.00E-124	Zinc finger, C3HC4 type (RING finger) containing protein~data source:Pfam, source key:PF00097, evidence:ISS~putative
172	2	438	2	1315	g13477235	1.00E-82	Similar to RIKEN cDNA 0610037N03 gene
173	1	106	1	318	g15741221	1.00E-17	gene overexpressed in astrocytoma
173	1	106	1	318	g458726	2.00E-13	estrogen responsive finger protein (efp)
173	1	106	1	318	g16877339	2.00E-13	zinc finger protein 147 (estrogen-responsive finger protein)
174	2	357	2	1072	g4239984	1.00E-143	insulin receptor substrate protein of 53 kDa (a shorter form)
174	2	357	2	1072	g4239982	1.00E-143	insulin receptor substrate protein of 53 kDa (a longer form)
174	2	357	2	1072	g4126477	1.00E-143	BAP2-beta protein
175	3	266	546	1343	g3327220	1.00E-123	KIAA0703 protein
175	3	266	546	1343	g19550878	1.00E-103	putative secretory pathway Ca-ATPase SPCA2
175	3	266	546	1343	g20072000	2.00E-99	Unknown (protein for IMAGE:4984604)
176	3	470	255	1664	g16033591	0.00	SH2 domain-containing phosphatase anchor protein 2b
176	3	470	255	1664	g18092655	0.00	immunoglobulin superfamily receptor translocation associated protein 3
176	3	470	255	1664	g16033588	0.00	SH2 domain-containing phosphatase anchor protein 2a
177	3	938	3	2816	g22597198	0.00	enaptin
177	3	938	3	2816	g24417709	0.00	nesprin-1
177	3	938	3	2816	g22597200	0.00	enaptin165 short isoform
178	3	928	21	2804	g13365845	0.00	hypothetical protein
178	3	928	21	2804	g4589506	0.00	KIAA0931 protein
178	3	928	21	2804	g20521103	0.00	KIAA0606 protein
179	2	304	2	913	g14198272	1.00E-139	Unknown (protein for MGC:5352)
179	2	304	2	913	g12848731	1.00E-123	data source:SPTR, source key:O46084, evidence:ISS~putative~related to EG:63B12.4 PROTEIN
179	2	304	2	913	g23820820	1.00E-63	Hypothetical protein R07G3.5
180	3	320	207	1166	g13185169	1.00E-170	unnamed protein product
180	3	320	207	1166	g17390445	1.00E-167	g1-related zinc finger protein
180	3	320	207	1166	g6175860	1.00E-167	g1-related zinc finger protein
181	2	358	218	1291	g21755898	0.00	unnamed protein product
181	2	358	218	1291	g18204012	0.00	Similar to RIKEN cDNA B830026H24 gene

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
181	2	358	218	1291	g12861800	0.00	data source:SPTR, source key:P97584, evidence:ISS-homolog to NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE (EC 1.1.1.-) (DITHIOLETHIONE-INDUCIBLE GENE-1)-putative
182	1	438	154	1467	g20521722	0.00	KIAA1004 protein
182	1	438	154	1467	g10440530	0.00	FLJ00115 protein
182	1	438	154	1467	g5917730	3.00E-92	F-box protein Ulna
183	1	246	280	1017	g21739365	1.00E-129	hypothetical protein
183	1	246	280	1017	g14424793	1.00E-127	Unknown (protein for MGC:15165)
183	1	246	280	1017	g4929679	1.00E-126	CGI-105 protein
184	3	266	354	1151	g4210363	1.00E-131	FUS glycine rich protein
184	3	266	354	1151	g386157	1.00E-131	TLS
184	3	266	354	1151	g3582784	1.00E-131	FUS/TLS protein
185	3	539	3	1619	g12275901	0.00	tripartite motif protein TRIM19 zeta
185	3	539	3	1619	g12275899	0.00	tripartite motif protein TRIM19 epsilon
185	3	539	3	1619	g12275897	0.00	tripartite motif protein TRIM19 delta
186	1	242	1	726	g21752509	1.00E-151	unnamed protein product
186	1	242	1	726	g22761208	9.00E-90	unnamed protein product
186	1	242	1	726	g5262557	1.00E-88	hypothetical protein
187	2	194	938	1519	g22760718	1.00E-116	unnamed protein product
187	2	194	938	1519	g21739830	1.00E-116	hypothetical protein
187	2	194	938	1519	g21618492	1.00E-116	Unknown (protein for MGC:45380)
188	1	149	145	591	g21336098	1.00E-84	unnamed protein product
188	1	149	145	591	g7959207	3.00E-26	KIAA1473 protein
188	1	149	145	591	g498736	4.00E-26	zinc finger protein
189	3	268	756	1559	g12314164	1.00E-151	bA526D8.2 (novel protein similar to KIAA1074)
189	3	268	756	1559	g12314195	1.00E-134	bA255A11.3 (novel protein similar to KIAA1074)
189	3	268	756	1559	g12053099	3.00E-96	hypothetical protein
190	3	1304	3	3914	g5931959	0.00	acinusL
190	3	1304	3	3914	g3327154	0.00	KIAA0670 protein
190	3	1304	3	3914	g9622185	0.00	acinusL protein
192	2	837	41	2551	g15917538	0.00	NG36/G9a
192	2	837	41	2551	g21832045	0.00	G9a short

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
192	2	837	41	2551	g21832049	0.00	G9a long
193	2	445	35	1369	g12857369	1.00E-123	data source:SPTR, source key:Q9UII4, evidence:ISS-homolog to CYCLIN-E BINDING PROTEIN 1-putative
193	2	445	35	1369	g12846911	1.00E-113	data source:SPTR, source key:Q9UII4, evidence:ISS-homolog to CYCLIN-E BINDING PROTEIN 1-putative
193	2	445	35	1369	g21750989	9.00E-97	unnamed protein product
194	1	139	532	948	g22760684	3.00E-50	unnamed protein product
194	1	139	532	948	g12858264	7.00E-48	data source:SPTR, source key:P70193, evidence:ISS-putative-similar to MEMBRANE GLYCOPROTEIN
194	1	139	532	948	g1545807	3.00E-31	membrane glycoprotein
195	2	650	287	2236	g10047251	0.00	KIAA1588 protein
195	2	650	287	2236	g16797866	0.00	ZNF317-4 protein
195	2	650	287	2236	g16797860	0.00	ZNF317-2 protein
196	1	157	1	471	g14250235	2.00E-17	RIKEN cDNA 4633401C23 gene
196	1	157	1	471	g12852573	2.00E-17	Zinc finger domain containing protein~data source:InterPro, source key:IPR000822, evidence:ISS-putative
196	1	157	1	471	g340446	3.00E-17	zinc finger protein 7 (ZFP7)
197	2	431	2	1294	g5738952	0.00	hTbr2
197	2	431	2	1294	g9711283	0.00	Tbr2
197	2	431	2	1294	g5738950	0.00	Tbr2
198	2	975	158	3082	g6959306	0.00	BOG25
198	2	975	158	3082	g21961541	0.00	expressed sequence A1594717
198	2	975	158	3082	g15126721	0.00	Similar to SH3-domain binding protein 4
199	1	484	1	1452	g24181967	0.00	NEW1 domain containing protein
199	1	484	1	1452	g24181969	0.00	NEW1 domain containing protein isoform
199	1	484	1	1452	g24181965	0.00	NEW1 domain containing protein
200	2	275	518	1342	g7022363	1.00E-160	unnamed protein product
200	2	275	518	1342	g4352515	1.00E-160	single-strand selective monofunctional uracil DNA glycosylase
200	2	275	518	1342	g19339024	1.00E-160	SMUG1
201	1	245	1	735	g23273536	3.00E-97	Unknown (protein for MGC:46523)
201	1	245	1	735	g22761212	3.00E-97	unnamed protein product
201	1	245	1	735	g22207737	3.00E-97	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
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202	2	247	527	1267	g7023136	1.00E-134	unnamed protein product
202	2	247	527	1267	g13278516	1.00E-101	Similar to hypothetical protein FLJ10846
203	2	749	1034	3280	g4239895	0.00	MASL1
203	2	749	1034	3280	g15559745	0.00	Similar to MFH-amplified sequences with leucine-rich tandem repeats 1
203	2	749	1034	3280	g19916243	3.00E-14	hypothetical protein
204	1	330	910	1899	g21756391	9.00E-27	unnamed protein product
205	1	301	133	1035	g20067239	1.00E-118	putative regulation protein GS3
205	1	301	133	1035	g12859941	3.00E-56	evidence:NAS~hypothetical protein~putative
205	1	301	133	1035	g5052516	7.00E-25	BcDNA.GH03108
206	1	213	1	639	g21739500	1.00E-08	hypothetical protein
206	1	213	1	639	g456269	3.00E-05	zinc finger protein 30
206	1	213	1	639	g12851705	3.00E-05	data source:MCD, source key:MGI:99178, evidence:ISS~putative~zinc finger protein 30
207	2	322	2	967	g155559324	1.00E-180	Unknown (protein for IMAGE:4309224)
207	2	322	2	967	g16551666	1.00E-173	unnamed protein product
207	2	322	2	967	g21739611	1.00E-109	hypothetical protein
208	3	238	381	1094	g21410798	1.00E-80	Unknown (protein for IMAGE:4396549)
208	3	238	381	1094	g19526448	2.00E-69	TRH4
208	3	238	381	1094	g21618502	4.00E-68	Similar to RIKEN cDNA 2310081H14 gene



TABLE 8

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less; Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6; Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less; Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less; Signal peptide hits: Score= 0 or greater

TABLE 8

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score $\geq$ GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.	

TABLE 8

Program	Description	Reference	Parameter Threshold
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

## CLAIMS

## What is claimed is:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group  
5 consisting of:
- a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104,
  - b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104,
  - c) a polynucleotide sequence complementary to a),
  - 10 d) a polynucleotide sequence complementary to b), and
  - e) an RNA equivalent of a) through d).
2. An isolated polynucleotide of claim 1, comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104.
- 15 3. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 1.
4. A composition for the detection of expression of disease detection and treatment molecule  
20 polynucleotides comprising at least one of the polynucleotides of claim 1 and a detectable label.
5. A method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a sequence of a polynucleotide of claim 1, the method comprising:
- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction  
25 amplification, and
  - b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.
6. A method for detecting a target polynucleotide in a sample, said target polynucleotide  
30 comprising a sequence of a polynucleotide of claim 1, the method comprising:
- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

7. A method of claim 5, wherein the probe comprises at least 30 contiguous nucleotides.

8. A method of claim 5, wherein the probe comprises at least 60 contiguous nucleotides.

9. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 1.

10. A cell transformed with a recombinant polynucleotide of claim 9.

11. A transgenic organism comprising a recombinant polynucleotide of claim 9.

12. A method for producing a disease detection and treatment molecule polypeptide, the method comprising:

a) culturing a cell under conditions suitable for expression of the disease detection and treatment molecule polypeptide, wherein said cell is transformed with a recombinant polynucleotide of claim 9, and

b) recovering the disease detection and treatment molecule polypeptide so expressed.

13. A purified disease detection and treatment molecule polypeptide (MDDT) encoded by at least one of the polynucleotides of claim 2.

14. An isolated antibody which specifically binds to a disease detection and treatment molecule polypeptide of claim 13.

15. A method of identifying a test compound which specifically binds to the disease detection and treatment molecule polypeptide of claim 13, the method comprising the steps of:

a) providing a test compound;

b) combining the disease detection and treatment molecule polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and

c) detecting binding of the disease detection and treatment molecule polypeptide to the test compound, thereby identifying the test compound which specifically binds the disease detection and treatment molecule polypeptide.

16. A microarray wherein at least one element of the microarray is a polynucleotide of claim 3.

17. A method for generating a transcript image of a sample which contains polynucleotides, the method comprising the steps of:

- a) labeling the polynucleotides of the sample,
- b) contacting the elements of the microarray of claim 16 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and
- c) quantifying the expression of the polynucleotides in the sample.

10

18. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 1, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

19. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 1 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 1 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

30

20. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first

oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target polynucleotide, said target polynucleotide having a sequence of claim 1.

21. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is  
5 completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

22. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 60 contiguous nucleotides of said target polynucleotide

10 23. An array of claim 20, which is a microarray.

24. An array of claim 20, further comprising said target polynucleotide hybridized to said first oligonucleotide or polynucleotide.

15 25. An array of claim 20, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

26. An array of claim 20, wherein each distinct physical location on the substrate contains multiple nucleotide molecules having the same sequence, and each distinct physical location on the  
20 substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at another physical location on the substrate.

27. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

25 a) an amino acid sequence selected from the group consisting of SEQ ID NO:105-208,

b) a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208,

c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and

30 d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

28. An isolated polypeptide of claim 27, comprising a polypeptide sequence selected from the group consisting of SEQ ID NO:105-208.

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&lt;400&gt; 3

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&lt;211&gt; 1560

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;400&gt; 4

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&lt;223&gt; Incyte ID No: LG:7685059.6:2002JAN18

&lt;400&gt; 5

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&lt;211&gt; 901

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:7689671.1:2002JAN18

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1) ... (901)

&lt;223&gt; a, t, c, g, or other

&lt;400&gt; 6

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<212> DNA

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&lt;211&gt; 3717

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;223&gt; Incyte ID No: LG:006394.31:2002JAN18

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&lt;223&gt; Incyte ID No: LG:1383494.16:2002JAN18

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&lt;400&gt; 37

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&lt;213&gt; Homo sapiens

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&lt;223&gt; Incyte ID No: LG:228273.22:2002JAN18

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&lt;211&gt; 222

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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:236767.26:2002JAN18

&lt;400&gt; 45

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;223&gt; Incyte ID No: LG:237489.7:2002JAN18

&lt;400&gt; 46

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;223&gt; Incyte ID No: LG:238218.20:2002JAN18

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&lt;223&gt; Incyte ID No: LG:253193.17:2002JAN18

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&lt;223&gt; Incyte ID No: LG:330985.1:2002JAN18

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&lt;211&gt; 3444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;223&gt; Incyte ID No: LG:402029.14:2002JAN18

&lt;220&gt;

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&lt;223&gt; a, t, c, g, or other

&lt;400&gt; 71

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&lt;211&gt; 2396

&lt;212&gt; DNA



&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;223&gt; Incyte ID No: LG:407233.2:2002JAN18

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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:407346.1:2002JAN18

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&lt;223&gt; Incyte ID No: LG:407689.7:2002JAN18

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&lt;213&gt; Homo sapiens

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&lt;223&gt; Incyte ID No: LG:407700.1:2002JAN18

&lt;220&gt;

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&lt;400&gt; 75

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;223&gt; Incyte ID No: LG:410461.92:2002JAN18

&lt;220&gt;

&lt;221&gt; unsure

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&lt;223&gt; a, t, c, g, or other

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&lt;220&gt;

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&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;211&gt; 2552

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:7763587.20:2002JAN18

&lt;400&gt; 88

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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:899263.10:2002JAN18

&lt;400&gt; 89

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&lt;213&gt; Homo sapiens

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&lt;223&gt; Incyte ID No: LG:977837.31:2002JAN18

&lt;400&gt; 90

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&lt;223&gt; Incyte ID No: LG:978560.13:2002JAN18

&lt;400&gt; 91

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&lt;211&gt; 1381

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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:979390.2:2002JAN18

&lt;400&gt; 92

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&lt;223&gt; Incyte ID No: LG:997202.7:2002JAN18

&lt;400&gt; 94

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&lt;213&gt; Homo sapiens

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&lt;223&gt; Incyte ID No: LG:998756.3:2002JAN18

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&lt;210&gt; 102

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:332474.7:2002JAN18

&lt;400&gt; 102

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&lt;210&gt; 103

&lt;211&gt; 1133

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:335727.8:2002JAN18

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<211> 6815

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Incyte ID No: LG:481983.1:2002JAN18

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&lt;210&gt; 105

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1447398.9.orf2:2002JAN18

&lt;400&gt; 105

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20     25     30
Arg Lys Leu Met Thr Gln Gly Gly Tyr Asp Met Val Gln Lys Leu
35     40     45
Phe Leu Asp Phe Phe Arg Arg Arg Leu Ser Gln Arg Pro Thr Ala
50     55     60
Glu Glu Leu Glu Gln Arg Asn Ile Leu Lys Pro Arg Asn Glu Gln
65     70     75
Glu Glu Gln Glu Glu Lys Arg Glu Ile Lys Arg Arg Leu Thr Arg
80     85     90
Lys Leu Ser Gln Arg Pro Thr Val Glu Glu Leu Arg Glu Arg Lys
95     100    105
Ile Leu Ile Arg Phe Ser Asp Tyr Val Glu Val Ala Asp Ala Gln
110    115    120
Asp Tyr Asp Arg Arg Ala Asp Lys Pro Trp Thr Arg Leu Thr Ala
125    130    135
Ala Asp Lys Ala Ala Ile Arg Lys Glu Leu Asn Glu Phe Lys Ser
140    145    150
Thr Glu Met Glu Val His Glu Leu Ser Arg His Leu Thr Arg Phe
155    160    165
His Arg Pro

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&lt;210&gt; 106

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:201488.3.orf3:2002JAN18

&lt;400&gt; 106

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          35          40          45
Thr Cys Asp Ser Cys Gly Arg Arg Leu Arg Gly Lys Ala Phe Tyr
          50          55          60
Asn Val Gly Glu Lys Val Tyr Cys Gln Glu Asp Phe Leu Tyr Ser
          65          70          75
Gly Phe Gln Gln Thr Ala Asp Lys Cys Ser Val Cys Gly His Leu
          80          85          90
Ile Met Glu Met Ile Leu Gln Ala Leu Gly Lys Ser Tyr His Pro
          95          100          105
Gly Cys Phe Arg Cys Ser Val Cys Asn Glu Cys Leu Asp Gly Val
          110          115          120
Pro Phe Thr Val Asp Val Glu Asn Asn Ile Tyr Cys Val Arg Asp
          125          130          135
Tyr His Thr Val Phe Ala Pro Lys Cys Ala Ser Cys Ala Arg Pro
          140          145          150
Ile Leu Pro Ala Gln Gly Cys Glu Thr Thr Ile Arg Val Val Ser
          155          160          165
Met Asp Arg Asp Tyr His Val Ala Cys Tyr His Cys Glu Asp Cys
          170          175          180
Gly Leu Gln Leu Ser Gly Glu Glu Gly Arg Arg Cys Tyr Pro Leu
          185          190          195
Ala Gly His Leu Leu Cys Arg Arg Cys His Leu Arg Arg Leu Gln
          200          205          210
Pro Gly Pro Leu Pro Ser Pro Thr Val His Val Thr Glu Leu
          215          220

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&lt;210&gt; 107

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:288410.6.orf2:2002JAN18

&lt;400&gt; 107

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          20          25          30
Tyr Ser Ser Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ala
          35          40          45
Leu Leu Gly Ala Thr Glu Tyr Ser Ser Glu Leu Asp Ile Trp Gly
          50          55          60
Ala Gly Cys Ile Phe Ile Glu Met Phe Gln Gly Gln Pro Leu Phe
          65          70          75
Pro Gly Val Ser Asn Ile Leu Glu Gln Leu Glu Lys Ile Trp Glu
          80          85          90
Val Leu Gly Val Pro Thr Glu Asp Thr Trp Pro Gly Val Ser Lys
          95          100          105
Leu Pro Asn Tyr Asn Pro Glu Trp Phe Pro Leu Pro Thr Pro Arg
          110          115          120
Ser Leu His Val Val Trp Asn Arg Leu Gly Arg Val Pro Glu Ala
          125          130          135
Glu Asp Leu Ala Ser Gln Met Leu Lys Gly Phe Pro Arg Asp Arg
          140          145          150
Val Ser Ala Gln Glu Ala Leu Val His Asp Tyr Phe Ser Ala Leu

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Pro Ser Gln Leu Tyr Gln Thr Ser  
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 170

<210> 108  
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<220>  
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 35 40 45  
 Val Pro Arg Arg Cys Arg Pro Arg Gly His His Ser Gly Gln Ala  
 50 55 60  
 Phe His Cys Ser Arg Ala Gln Arg Leu Leu Gly Glu Gln Asp Gln  
 65 70 75  
 Gln Ala Pro His His Pro Leu Gln Gly Asp Arg Pro Leu Gln Leu  
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 95 100 105  
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 110 115 120  
 Ile Asp Asp Cys Tyr Thr Ser Ala Arg Ser Cys Thr Ala Thr Leu  
 125 130 135  
 Gly Asn Phe Ala Lys Thr Thr Phe Asp Ala Ile Ser Ile Asp Leu  
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 Gln Leu Pro Asp Pro Arg Pro Leu Glu Glu Asp Cys Val His Gln  
 155 160 165  
 Val Ser Leu

<210> 109  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 35 40 45  
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 95 100 105

His Val Ser Gly Glu Pro Ser Thr Cys Arg Glu Val Gly Lys Asp  
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 140 145 150  
 Arg Gly Lys Thr His Cys Asn Cys Gly Glu His Thr Lys Ala Phe  
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<220>  
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 65 70

<210> 111  
 <211> 182  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:7689684.1.orf2:2002JAN18

<400> 111  
 Pro Lys Gln Gly Ile Arg Val Trp Ser Pro Arg His Pro Glu Asn  
 1 5 10 15  
 Phe Leu Gly Ile Glu Ser Arg Pro Pro Val Leu Ser Leu Ser Pro  
 20 25 30  
 Ile Leu Leu Tyr Thr Cys Glu Met Phe Gln Asp Pro Val Ala Phe  
 35 40 45  
 Asp Asp Val Ala Val Asn Phe Thr Gln Glu Glu Trp Ala Leu Leu  
 50 55 60  
 Asp Ile Ser Gln Arg Lys Leu Tyr Lys Glu Val Met Leu Glu Thr  
 65 70 75  
 Phe Arg Asn Leu Thr Ser Val Gly Lys Ser Trp Lys Asp Gln Asn  
 80 85 90  
 Ile Glu Tyr Glu Tyr Gln Asn Pro Arg Arg Asn Phe Arg Ser Leu  
 95 100 105  
 Ile Glu Lys Lys Val Asn Glu Ile Lys Asp Asp Ser His Cys Gly  
 110 115 120  
 Glu Thr Phe Thr Gln Val Pro Asp Asp Arg Leu Asn Phe Gln Glu  
 125 130 135  
 Lys Lys Ala Ser Pro Glu Ile Lys Ser Cys Asp Ser Phe Val Cys

	140		145		150
Gly Glu Val Gly	Leu Gly Asn Ser Ser	Phe Asn Met Asn Ile	Arg		
	155		160		165
Gly Asp Ile Gly	His Lys Ala Tyr Glu	Tyr Gln Glu Tyr Gly	Pro		
	170		175		180
Lys Pro					

<210> 112  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:7762669.1.orf1:2002JAN18

<400> 112

Val Ser Thr Phe Leu	Phe Trp Thr Tyr Gly Met Phe Gln Asp Ser	
1	5	10 15
Val Ala Phe Glu Asp	Val Ala Val Asn Phe Thr His Glu Glu Trp	
	20	25 30
Ala Leu Leu Gly Pro	Ser Gln Lys Asn Leu Tyr Arg Asp Val Met	
	35	40 45
Leu Glu Asn Phe Gln	Asn Leu Ala Ser Leu Gly Tyr Pro Leu His	
	50	55 60
Thr Pro His Leu Ile	Ser Gln Trp Glu Gln Glu Glu Asp Leu Gln	
	65	70 75
Thr Val Lys Arg Glu	Leu Ile Gln Gly Ile Phe Met Gly Glu His	
	80	85 90
Arg Glu Gly Lys Asn	Pro Trp Glu Lys Leu Phe Trp Leu Gly Glu	
	95	100 105
Lys Ile Asn		

<210> 113  
 <211> 240  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:965822.1.orf1:2002JAN18

<400> 113

Pro Arg Ser Ser Arg	Arg Val Trp Ala Ala Tyr Thr Glu Gly Lys	
1	5	10 15
Lys Lys Pro Ser Phe	Leu Gly Lys Cys Arg Lys Pro Ala Ser Gly	
	20	25 30
Arg Ser Leu Arg Ser	Pro Gln Gly Gly Ala Leu Ala Ala Gln Arg	
	35	40 45
Ala Arg Phe Pro Ala	Gly Glu Pro Arg Asn Gly Gly Ala Gly Gly	
	50	55 60
Gly Asp Ser Glu Asp	Pro Arg Leu Gly Phe Pro Thr Trp Ile Arg	
	65	70 75
Ser Ala Trp Gly Phe	Asp Pro His Pro Gly Ala Ala Pro Arg Arg	
	80	85 90
Ser Trp Ala Ala Arg	Ala Phe Gly Leu Arg His Arg Gln Arg His	
	95	100 105
Leu Glu Ala Gly Ala	Ser Gly Arg Leu Cys Leu Thr Cys Leu Leu	
	110	115 120
Glu Gly Asn Thr Gly	Lys Pro Gly Leu Ala Val Thr Leu Val Thr	
	125	130 135

Asn	Met	Ser	Gln	Asp	Ser	Val	Thr	Phe	Ala	Asp	Val	Ala	Val	Asn
				140					145					150
Phe	Thr	Lys	Glu	Glu	Trp	Thr	Leu	Leu	Asp	Pro	Ala	Gln	Arg	Asn
				155					160					165
Leu	Tyr	Arg	Asp	Val	Met	Leu	Glu	Asn	Ser	Arg	Asn	Leu	Ala	Phe
				170					175					180
Ile	Asp	Trp	Ala	Thr	Pro	Cys	Lys	Thr	Lys	Asp	Ala	Thr	Pro	Gln
				185					190					195
Pro	Asp	Ile	Leu	Pro	Lys	Arg	Thr	Phe	Pro	Glu	Ala	Asn	Arg	Val
				200					205					210
Cys	Leu	Thr	Ser	Ile	Arg	Phe	Pro	Ala	Leu	His	Ile	Lys	Arg	Arg
				215					220					225
Leu	Glu	Met	Pro	Gln	Asn	Arg	Gly	Thr	Thr	Gln	Ala	Gly	Gly	Glu
				230					235					240

&lt;210&gt; 114

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:006394.31.orf2:2002JAN18

&lt;400&gt; 114

Gly	Lys	Arg	Gly	Leu	Phe	Ala	Glu	Gly	Leu	Gln	Ala	Met	Pro	Val
1				5					10					15
Gly	Ser	Ala	Phe	Arg	Val	Pro	Cys	Pro	Ile	Leu	Glu	Gly	Pro	Ala
				20					25					30
Ala	Gly	Ser	Arg	Pro	Arg	Leu	Ser	Glu	Ala	Met	Gly	Ile	Gln	Ser
				35					40					45
Ala	Glu	Leu	Pro	Pro	Glu	Glu	Ser	Asp	Ser	Ser	Arg	Val	Asp	Phe
				50					55					60
Gly	Ser	Ser	Glu	Arg	Leu	Gly	Ser	Trp	Gln	Glu	Lys	Glu	Glu	Asp
				65					70					75
Ala	Arg	Pro	Asn	Ala	Ala	Ala	Pro	Ala	Leu	Gly	Pro	Val	Gly	Leu
				80					85					90
Glu	Ser	Asp	Leu	Ser	Lys	Val	Arg	His	Lys	Leu	Arg	Lys	Phe	Leu
				95					100					105
Gln	Arg	Arg	Pro	Thr	Leu	Gln	Ser	Leu	Arg	Glu	Lys	Gly	Tyr	Ile
				110					115					120
Lys	Asp	Gln	Val	Phe	Gly	Cys	Ala	Leu	Ala	Ala	Leu	Cys	Glu	Arg
				125					130					135
Glu	Arg	Ser	Arg	Val	Pro	Arg	Phe	Val	Gln	Gln	Cys	Ile	Arg	Ala
				140					145					150
Val	Glu	Ala	Arg	Gly	Leu	Asp	Ile	Asp	Gly	Leu	Tyr	Arg	Ile	Ser
				155					160					165
Gly	Asn	Leu	Ala	Thr	Ile	Gln	Lys	Leu	Arg	Tyr	Lys	Val	Asp	His
				170					175					180
Asp	Glu	Arg	Leu	Asp	Leu	Asp	Asp	Gly	Arg	Trp	Glu	Asp	Val	His
				185					190					195
Val	Ile	Thr	Gly	Ala	Leu	Lys	Leu	Phe	Phe	Arg	Glu	Leu	Pro	Glu
				200					205					210
Pro	Leu	Phe	Pro	Phe	Ser	His	Phe	Arg	Gln	Phe	Ile	Ala	Ala	Ile
				215					220					225
Lys	Leu	Gln	Asp	Gln	Ala	Arg	Arg	Ser	Arg	Cys	Val	Arg	Asp	Leu
				230					235					240
Val	Arg	Ser	Leu	Pro	Ala	Pro	Asn	His	Asp	Thr	Leu	Arg	Met	Leu
				245					250					255
Phe	Gln	His	Leu	Cys	Arg	Val	Ile	Glu	His	Gly	Glu	Gln	Asn	Arg
				260					265					270
Met	Ser	Val	Gln	Ser	Val	Ala	Ile	Val	Phe	Gly	Pro	Thr	Leu	Leu

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	275	280	285
Arg Pro Glu Val	Glu Glu Thr Ser Met	Pro Met Thr Met Val	Phe
	290	295	300
Gln Asn Gln Val	Val Glu Leu Ile Leu	Gln Gln Cys Ala Asp	Ile
	305	310	315
Phe Pro Pro His			

<210> 115  
 <211> 263  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:018258.1.orf2:2002JAN18

<400> 115	
Gly Cys Asp Val Arg	Leu Gln Thr Met Tyr Phe Leu Thr Pro Ile
1	5 10 15
Leu Val Ala Ile Leu	Cys Val Leu Val Val Trp Ile Phe Lys Asn
	20 25 30
Ala Asp Arg Ser Met	Glu Lys Lys Lys Gly Glu Pro Arg Thr Arg
	35 40 45
Ala Glu Ala Arg Pro	Trp Val Asp Glu Asp Leu Lys Asp Ser Ser
	50 55 60
Asp Leu His Gln Ala	Glu Glu Asp Ala Asp Glu Trp Gln Glu Ser
	65 70 75
Glu Glu Asn Val Glu	His Ile Pro Phe Ser His Asn His Tyr Pro
	80 85 90
Glu Lys Glu Met Val	Lys Arg Ser Gln Glu Phe Tyr Glu Leu Leu
	95 100 105
Asn Lys Arg Arg Ser	Val Arg Phe Ile Ser Asn Glu Gln Val Pro
	110 115 120
Met Glu Val Ile Asp	Asn Val Ile Arg Thr Ala Gly Thr Ala Pro
	125 130 135
Ser Gly Ala His Thr	Glu Pro Trp Thr Phe Val Val Val Lys Asp
	140 145 150
Pro Asp Val Lys His	Lys Ile Arg Lys Ile Ile Glu Glu Glu Glu
	155 160 165
Glu Ile Asn Tyr Met	Lys Arg Met Gly His Arg Trp Val Thr Asp
	170 175 180
Leu Lys Lys Leu Arg	Thr Asn Trp Ile Lys Glu Tyr Leu Asp Thr
	185 190 195
Ala Pro Ile Leu Ile	Leu Ile Phe Lys Gln Val His Gly Phe Ala
	200 205 210
Ala Asn Gly Lys Lys	Lys Val His Tyr Tyr Asn Glu Ile Ser Val
	215 220 225
Ser Ile Ala Cys Gly	His Pro Ala Ser Cys Pro Ala Glu Cys Ser
	230 235 240
Leu Val Thr Val Thr	Asn Asn Pro Leu Asn Val Ala Ser Asp Glu
	245 250 255
Gly Cys Pro Trp Ala	Ala Arg Thr
	260

<210> 116  
 <211> 449  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:027320.5.orf3:2002JAN18

<400> 116  
 Gly Glu Ala Gly Arg Ala Pro Asp Ser Asp Gly Gly Ser Asp Ala  
 1 5 10 15  
 Asp Ser Glu Val Gly Pro Gly Ser Pro Thr Arg Thr Ala Glu Ala  
 20 25 30  
 Ala Glu Glu Glu Met Ala Gly Pro Asn Gln Leu Cys Ile Arg Arg  
 35 40 45  
 Trp Thr Thr Lys His Val Ala Val Trp Leu Lys Asp Glu Gly Phe  
 50 55 60  
 Phe Glu Tyr Val Asp Ile Leu Cys Asn Lys His Arg Leu Asp Gly  
 65 70 75  
 Ile Thr Leu Leu Thr Leu Thr Glu Tyr Asp Leu Arg Ser Pro Pro  
 80 85 90  
 Leu Glu Ile Lys Val Leu Gly Asp Ile Lys Arg Leu Met Leu Ser  
 95 100 105  
 Val Arg Lys Leu Gln Lys Ile His Ile Asp Val Leu Glu Glu Met  
 110 115 120  
 Gly Tyr Asn Ser Asp Ser Pro Met Gly Ser Met Thr Pro Phe Ile  
 125 130 135  
 Ser Ala Leu Gln Ser Thr Asp Trp Leu Cys Asn Gly Glu Leu Ser  
 140 145 150  
 His Asp Cys Asp Gly Pro Ile Thr Asp Leu Asn Ser Asp Gln Tyr  
 155 160 165  
 Gln Tyr Met Asn Gly Lys Asn Lys His Ser Val Arg Arg Leu Asp  
 170 175 180  
 Pro Glu Tyr Trp Lys Thr Ile Leu Ser Cys Ile Tyr Val Phe Ile  
 185 190 195  
 Val Phe Gly Phe Thr Ser Phe Ile Met Val Ile Val His Glu Arg  
 200 205 210  
 Val Pro Asp Met Gln Thr Tyr Pro Pro Leu Pro Asp Ile Phe Leu  
 215 220 225  
 Asp Ser Val Pro Arg Ile Pro Trp Ala Phe Ala Met Thr Glu Val  
 230 235 240  
 Cys Gly Met Ile Leu Cys Tyr Ile Trp Leu Leu Val Leu Leu Leu  
 245 250 255  
 His Lys His Arg Ser Ile Leu Leu Arg Arg Leu Cys Ser Leu Met  
 260 265 270  
 Gly Thr Val Phe Leu Leu Arg Cys Phe Thr Met Phe Val Thr Ser  
 275 280 285  
 Leu Ser Val Pro Gly Gln His Leu Gln Cys Thr Gly Lys Ile Tyr  
 290 295 300  
 Gly Ser Val Trp Glu Lys Leu His Arg Ala Phe Ala Ile Trp Ser  
 305 310 315  
 Gly Phe Gly Met Thr Leu Thr Gly Val His Thr Cys Gly Asp Tyr  
 320 325 330  
 Met Phe Ser Gly His Thr Val Val Leu Thr Met Leu Asn Phe Phe  
 335 340 345  
 Val Thr Glu Tyr Thr Pro Arg Ser Trp Asn Phe Leu His Thr Leu  
 350 355 360  
 Ser Trp Val Leu Asn Leu Phe Gly Ile Phe Phe Ile Leu Ala Ala  
 365 370 375  
 His Glu His Tyr Ser Ile Asp Val Phe Ile Ala Phe Tyr Ile Thr  
 380 385 390  
 Thr Arg Leu Phe Leu Tyr Tyr His Thr Leu Ala Asn Thr Arg Ala  
 395 400 405  
 Tyr Gln Gln Ser Arg Arg Ala Arg Ile Trp Phe Pro Met Phe Ser  
 410 415 420  
 Phe Phe Glu Cys Asn Val Asn Gly Thr Val Pro Asn Glu Tyr Cys  
 425 430 435  
 Trp Pro Phe Ser Lys Pro Ala Ile Met Lys Arg Leu Ile Gly  
 440 445

&lt;210&gt; 117

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<211> 601  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:057499.1.orf1:2002JAN18

<400> 117  
 Gln Gln His Pro Arg Gln Ala Ala Pro Gln Met Leu Gln Gln Gln 15  
 1 5 10  
 Pro Pro Arg Leu Ile Ser Val Gln Thr Met Gln Arg Gly Asn Met 30  
 20 25  
 Asn Cys Gly Ala Phe Gln Ala His Gln Met Arg Leu Ala Gln Asn 45  
 35 40  
 Ala Ala Arg Ile Pro Gly Ile Pro Arg His Ser Gly Pro Gln Tyr 60  
 50 55  
 Ser Met Met Gln Pro His Leu Gln Arg Gln His Ser Asn Pro Gly 75  
 65 70  
 His Ala Gly Pro Phe Pro Val Val Ser Val His Asn Thr Thr Ile 90  
 80 85  
 Asn Pro Thr Ser Pro Thr Thr Ala Thr Met Ala Asn Ala Asn Arg 105  
 95 100  
 Gly Pro Thr Ser Pro Ser Val Thr Ala Ile Glu Leu Ile Pro Ser 120  
 110 115  
 Val Thr Asn Pro Glu Asn Leu Pro Ser Leu Pro Asp Ile Pro Pro 135  
 125 130  
 Ile Gln Ala Asn Val Val Pro Met Met His Ser Trp Tyr Glu Phe 150  
 140 145  
 Gly Ala Arg Glu Lys Thr Gln Asp Gln Asn Val Leu Glu Asp Ala 165  
 155 160  
 Gly Ser Ser Ser Leu Asp Asn Leu Leu Ser Arg Tyr Ile Ser Gly 180  
 170 175  
 Ser His Leu Pro Pro Gln Pro Thr Ser Thr Met Asn Pro Ser Pro 195  
 185 190  
 Gly Pro Ser Ala Leu Ser Pro Gly Ser Ser Gly Leu Ser Asn Ser 210  
 200 205  
 His Thr Pro Val Arg Pro Pro Ser Thr Ser Ser Thr Gly Ser Arg 225  
 215 220  
 Gly Ser Cys Gly Ser Ser Gly Arg Thr Ala Glu Lys Thr Ser Leu 240  
 230 235  
 Ser Phe Lys Ser Asp Gln Val Lys Val Lys Gln Glu Pro Gly Thr 255  
 245 250  
 Glu Asp Glu Ile Cys Ser Phe Ser Gly Gly Val Lys Gln Glu Lys 270  
 260 265  
 Thr Glu Asp Gly Arg Arg Ser Ala Cys Met Leu Ser Ser Pro Glu 285  
 275 280  
 Ser Ser Leu Thr Pro Pro Leu Ser Thr Asn Leu His Leu Glu Ser 300  
 290 295  
 Glu Leu Asp Ala Leu Ala Ser Leu Glu Asn His Val Lys Ile Glu 315  
 305 310  
 Pro Ala Asp Met Asn Glu Ser Cys Lys Gln Ser Gly Leu Ser Ser 330  
 320 325  
 Leu Val Asn Gly Lys Ser Pro Ile Arg Ser Leu Met His Arg Ser 345  
 335 340  
 Ala Arg Ile Gly Gly Asp Gly Asn Asn Lys Asp Asp Asp Pro Asn 360  
 350 355  
 Glu Asp Trp Cys Ala Val Cys Gln Asn Gly Gly Asp Leu Leu Cys 375  
 365 370  
 Cys Glu Lys Cys Pro Lys Val Phe His Leu Thr Cys His Val Pro 390  
 380 385  
 Thr Leu Leu Ser Phe Pro Ser Gly Asp Trp Ile Cys Thr Phe Cys 405  
 395 400

Arg Asp Ile Gly Lys Pro Glu Val Glu Tyr Asp Cys Asp Asn Leu  
 410 415 420  
 Gln His Ser Lys Lys Gly Lys Thr Ala Gln Gly Leu Ser Pro Val  
 425 430 435  
 Asp Gln Arg Lys Cys Glu Arg Leu Leu Leu Tyr Leu Tyr Cys His  
 440 445 450  
 Glu Leu Ser Ile Glu Phe Gln Glu Pro Val Pro Ala Ser Ile Pro  
 455 460 465  
 Asn Tyr Tyr Lys Ile Ile Lys Lys Pro Met Asp Leu Ser Thr Val  
 470 475 480  
 Lys Lys Lys Leu Gln Lys Lys His Ser Gln His Tyr Gln Ile Pro  
 485 490 495  
 Asp Asp Phe Val Ala Asp Val Arg Leu Ile Phe Lys Asn Cys Glu  
 500 505 510  
 Arg Phe Asn Glu Met Met Lys Val Val Gln Val Tyr Ala Asp Thr  
 515 520 525  
 Gln Glu Ile Asn Leu Lys Ala Asp Ser Glu Val Ala Gln Ala Gly  
 530 535 540  
 Lys Ala Val Ala Leu Tyr Phe Glu Asp Lys Leu Thr Glu Ile Tyr  
 545 550 555  
 Ser Asp Arg Thr Phe Ala Pro Leu Pro Glu Phe Glu Gln Glu Glu  
 560 565 570  
 Asp Asp Gly Glu Val Thr Glu Asp Ser Asp Glu Asp Phe Ile Gln  
 575 580 585  
 Pro Arg Arg Lys Arg Leu Lys Ser Asp Glu Arg Pro Val His Ile  
 590 595 600  
 Lys

<210> 118  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:065935.21.orf2:2002JAN18

<400> 118  
 Phe Leu His Tyr His Pro Pro Pro Thr Gln Gly Trp Trp Trp Arg  
 1 5 10 15  
 Lys Met Ala Ala Ala Trp Gly Ser Ser Leu Thr Ala Ala Thr Gln  
 20 25 30  
 Arg Ala Val Thr Pro Trp Pro Arg Gly Arg Leu Leu Thr Ala Ser  
 35 40 45  
 Leu Gly Pro Gln Ala Arg Arg Glu Ala Ser Ser Ser Ser Pro Glu  
 50 55 60  
 Ala Gly Glu Gly Gln Ile Arg Leu Thr Asp Ser Cys Val Gln Arg  
 65 70 75  
 Leu Leu Glu Ile Thr Glu Gly Ser Glu Phe Leu Arg Leu Gln Val  
 80 85 90  
 Glu Gly Gly Gly Cys Ser Gly Phe Gln Tyr Lys Phe Ser Leu Asp  
 95 100 105  
 Thr Val Ile Asn Pro Asp Asp Arg Val Phe Glu Gln Gly Gly Ala  
 110 115 120  
 Arg Val Val Val Asp Ser Asp Ser Leu Ala Phe Val Lys Gly Ala  
 125 130 135  
 Gln Val Asp Phe Ser Gln Glu Leu Ile Arg Ser Ser Phe Gln Val  
 140 145 150  
 Leu Asn Asn Pro Gln Ala Gln Gln Gly Cys Ser Cys Gly Ser Ser  
 155 160 165  
 Phe Ser Ile Lys Leu  
 170

<210> 119  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:071860.12.orf3:2002JAN18

<400> 119  
 Val Cys Arg Asn Ser Tyr Phe Tyr Leu Pro Ser Leu Ser Glu Ser  
 1 5 10 15  
 Lys His Cys Leu Arg Ile Gln His Thr Phe Cys Phe Leu Thr Cys  
 20 25 30  
 Val Gln Ala Tyr Val His Lys Ser Val Met Glu Glu Leu Lys Arg  
 35 40 45  
 Ile Ile Asp Asp Ser Glu Ile Thr Lys Glu Asp Asp Ala Leu Trp  
 50 55 60  
 Pro Pro Pro Asp Arg Val Gly Arg Gln Glu Leu Glu Ile Val Ile  
 65 70 75  
 Gly Asp Glu His Ile Ser Phe Thr Thr Ser Lys Ile Gly Ser Leu  
 80 85 90  
 Ile Asp Val Asn Gln Ser Lys Asp Pro Glu Gly Leu Arg Val Phe  
 95 100 105  
 Tyr

<210> 120  
 <211> 334  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:087383.29.orf2:2002JAN18

<400> 120  
 Val Tyr Phe Ala Ala Pro Ser Ala Phe Glu Lys Met Ser Val Thr  
 1 5 10 15  
 Tyr Asp Asp Ser Val Gly Val Glu Val Ser Ser Asp Ser Phe Trp  
 20 25 30  
 Glu Val Gly Asn Tyr Lys Arg Thr Val Lys Arg Ile Asp Asp Gly  
 35 40 45  
 His Arg Leu Cys Ser Asp Leu Met Asn Cys Leu His Glu Arg Ala  
 50 55 60  
 Arg Ile Glu Lys Ala Tyr Ala Gln Gln Leu Thr Glu Trp Ala Arg  
 65 70 75  
 Arg Trp Arg Gln Leu Val Glu Lys Gly Pro Gln Tyr Gly Thr Val  
 80 85 90  
 Glu Lys Ala Trp Met Ala Phe Met Ser Glu Ala Glu Arg Val Ser  
 95 100 105  
 Glu Leu His Leu Glu Val Lys Ala Ser Leu Met Asn Asp Asp Phe  
 110 115 120  
 Glu Lys Ile Lys Asn Trp Gln Lys Glu Ala Phe His Lys Gln Met  
 125 130 135  
 Met Gly Gly Phe Lys Glu Thr Lys Glu Ala Glu Asp Gly Phe Arg  
 140 145 150  
 Lys Ala Gln Lys Pro Trp Ala Lys Lys Leu Lys Glu Val Glu Ala  
 155 160 165  
 Ala Lys Lys Ala His His Ala Ala Cys Lys Glu Glu Lys Leu Ala  
 170 175 180  
 Ile Ser Arg Glu Ala Asn Ser Lys Ala Asp Pro Ser Leu Asn Pro  
 185 190 195

Glu	Gln	Leu	Lys	Lys	Leu	Gln	Asp	Lys	Ile	Glu	Lys	Cys	Lys	Gln
				200					205					210
Asp	Val	Leu	Lys	Thr	Lys	Glu	Lys	Tyr	Glu	Lys	Ser	Leu	Lys	Glu
				215					220					225
Leu	Asp	Gln	Gly	Thr	Pro	Gln	Tyr	Met	Glu	Asn	Met	Glu	Gln	Val
				230					235					240
Phe	Glu	Gln	Cys	Gln	Gln	Phe	Glu	Glu	Lys	Arg	Leu	Arg	Phe	Phe
				245					250					255
Arg	Glu	Val	Leu	Leu	Glu	Val	Gln	Lys	His	Leu	Asp	Leu	Ser	Asn
				260					265					270
Val	Ala	Gly	Tyr	Lys	Ala	Ile	Tyr	His	Asp	Leu	Glu	Gln	Ser	Ile
				275					280					285
Arg	Ala	Ala	Asp	Ala	Val	Glu	Asp	Leu	Arg	Trp	Phe	Arg	Ala	Asn
				290					295					300
His	Gly	Pro	Gly	Met	Ala	Met	Asn	Trp	Pro	Gln	Phe	Glu	Val	Arg
				305					310					315
Gly	Gly	Cys	Ala	His	Glu	Leu	Val	Ser	Leu	Glu	Glu	Asp	Leu	Gly
				320					325					330
Pro	Gln	Ser	Cys											

&lt;210&gt; 121

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:098580.3.orf2:2002JAN18

&lt;400&gt; 121

Gln	Trp	Lys	Lys	Pro	Val	Gln	Ile	Leu	Met	Val	Gly	Ser	Cys	Lys
1				5					10					15
Val	Thr	Ser	Val	Met	Met	Leu	Leu	Gln	Arg	Leu	Met	Trp	Glu	Lys
				20					25					30
Asp	Phe	Ile	Ala	Phe	Lys	Ser	Ser	Thr	Pro	His	Asn	Val	Ser	Trp
				35					40					45
Arg	His	Glu	Thr	Asn	Gly	Ser	Val	Phe	Ile	Ser	Gln	Ile	Ile	Tyr
				50					55					60
Tyr	Phe	Arg	Glu	Tyr	Ser	Trp	Ser	His	His	Leu	Glu	Glu	Ile	Phe
				65					70					75
Gln	Lys	Val	Gln	His	Ser	Phe	Glu	Thr	Pro	Asn	Ile	Leu	Thr	Gln
				80					85					90
Leu	Pro	Thr	Ile	Glu	Arg	Leu	Ser	Met	Thr	Arg	Tyr	Phe	Tyr	Leu
				95					100					105
Phe	Pro	Gly	Asn											

&lt;210&gt; 122

&lt;211&gt; 519

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1001879.1.orf1:2002JAN18

&lt;400&gt; 122

Arg	Ala	Ala	Val	Leu	Gly	Arg	Val	Arg	Gly	Gly	Leu	Ala	Ala	Glu
1				5					10					15
Ala	Pro	Arg	Arg	Gly	Ala	Asn	Gly	Ala	Asn	Ala	Ala	Arg	Ser	Pro
				20					25					30
Pro	Ala	Arg	Arg	Cys	Ala	Gly	Gly	Trp	Trp	Arg	Gly	Pro	Arg	Pro

	35		40		45
Thr Leu Arg Thr Met	Thr Cys Trp Leu Cys	Val Leu Ser Leu Pro			
50	55	60			
Leu Leu Leu Leu Pro	Ala Ala Pro Pro Pro	Ala Gly Gly Cys Pro			
65	70	75			
Ala Arg Cys Glu Cys	Thr Val Gln Thr Arg	Ala Val Ala Cys Thr			
80	85	90			
Arg Arg Arg Leu Thr	Ala Val Pro Asp Gly	Ile Pro Ala Glu Thr			
95	100	105			
Arg Leu Leu Glu Leu	Ser Arg Asn Arg Ile	Arg Cys Leu Asn Pro			
110	115	120			
Gly Asp Leu Ala Ala	Leu Pro Ala Leu Glu	Glu Leu Asp Leu Ser			
125	130	135			
Glu Asn Ala Ile Ala	His Val Glu Pro Gly	Ala Phe Ala Asn Leu			
140	145	150			
Pro Arg Leu Arg Val	Leu Arg Leu Arg Gly	Asn Gln Leu Lys Leu			
155	160	165			
Ile Pro Pro Gly Val	Phe Thr Arg Leu Asp	Asn Leu Thr Leu Leu			
170	175	180			
Asp Leu Ser Glu Asn	Lys Leu Val Ile Leu	Leu Asp Tyr Thr Phe			
185	190	195			
Gln Asp Leu His Ser	Leu Arg Arg Leu Glu	Val Gly Asp Asn Asp			
200	205	210			
Leu Val Phe Val Ser	Arg Arg Ala Phe Ala	Gly Leu Leu Ala Leu			
215	220	225			
Glu Glu Leu Thr Leu	Glu Arg Cys Asn Leu	Thr Ala Leu Ser Gly			
230	235	240			
Glu Ser Leu Gly His	Leu Arg Ser Leu Gly	Ala Leu Arg Leu Arg			
245	250	255			
His Leu Ala Ile Ala	Ser Leu Glu Asp Gln	Asn Phe Arg Arg Leu			
260	265	270			
Pro Gly Leu Leu His	Leu Glu Ile Ala Gln	Leu Ala Ala Ala Gly			
275	280	285			
Arg Gln Val Ala Ala	Gly Ser Leu Arg Gly	Leu Asn Leu Thr Ser			
290	295	300			
Leu Ser Val Thr His	Thr Asn Ile Thr Ala	Val Pro Ala Ala Ala			
305	310	315			
Leu Arg His Gln Ala	His Leu Thr Cys Leu	Asn Leu Ser His Asn			
320	325	330			
Pro Ile Ser Thr Val	Pro Arg Gly Ser Phe	Arg Asp Leu Val Arg			
335	340	345			
Leu Arg Glu Leu His	Leu Ala Gly Ala Leu	Leu Ala Val Val Glu			
350	355	360			
Pro Gln Ala Phe Leu	Gly Leu Arg Gln Ile	Arg Leu Leu Asn Leu			
365	370	375			
Ser Asn Asn Leu Leu	Ser Thr Leu Glu Ser	Thr Phe His Ser			
380	385	390			
Val Asn Thr Leu Glu	Thr Leu Arg Val Asp	Gly Asn Pro Leu Ala			
395	400	405			
Cys Asp Cys Arg Leu	Leu Trp Ile Val Gln	Arg Arg Lys Thr Leu			
410	415	420			
Asn Phe Asp Gly Arg	Leu Pro Ala Cys Ala	Thr Pro Ala Glu Val			
425	430	435			
Arg Gly Asp Ala Leu	Arg Asn Leu Pro Asp	Ser Val Leu Phe Glu			
440	445	450			
Tyr Phe Val Cys Arg	Lys Pro Lys Ile Arg	Glu Arg Arg Leu Gln			
455	460	465			
Arg Val Thr Ala Thr	Ala Gly Glu Asp Val	Arg Phe Leu Cys Arg			
470	475	480			
Ala Glu Gly Glu Pro	Ala Pro Thr Val Ala	Trp Val Thr Pro Gln			
485	490	495			
His Arg Pro Val Thr	Ala Thr Ser Ala Gly	Arg Ala Arg Val Leu			
500	505	510			

Pro Gly Gly Thr Leu Glu Ile Gln Asp  
515

<210> 123  
<211> 132  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte ID No: LG:1079456.4.orf3:2002JAN18

<400> 123  
Gly Asp Pro Pro Arg Pro Gly Phe Cys Pro Ala Arg Ala Asp Ser  
1 5 10 15  
Arg Lys Ser Gly Ser Gly Ser Arg Gly Val Thr Val Thr Pro Arg  
20 25 30  
Arg Ile Asn Ser Gln Arg Leu Met Leu His Glu Lys Ala Thr Lys  
35 40 45  
Lys Thr Lys Glu Lys Glu Thr Arg Met Ala Leu Pro Gln Gly Cys  
50 55 60  
Leu Thr Phe Lys Asp Val Ala Ile Glu Phe Ser Leu Glu Glu Trp  
65 70 75  
Lys Cys Leu Asn Pro Ala Gln Arg Ala Leu Tyr Arg Ala Val Met  
80 85 90  
Leu Glu Asn Tyr Arg Asn Leu Glu Ser Val Gly Leu Thr Ser Lys  
95 100 105  
Asp Ser Trp Tyr Met Arg Lys Lys Pro Gly Arg Gly Arg Gly Lys  
110 115 120  
Gln Arg Arg Gln Glu Trp Phe Phe Leu Arg Val Tyr  
125 130

<210> 124  
<211> 524  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte ID No: LG:1080598.9.orf2:2002JAN18

<400> 124  
Pro Cys Thr Lys Arg Asn Gly Asp Cys Leu Tyr Pro Pro Arg Phe  
1 5 10 15  
Ile Ser Trp Pro Glu Val Ile Leu Ala Ser Arg Lys Gly Cys Thr  
20 25 30  
Ser Ser His His Gln Leu Gln Arg Met Ala Ala Ile Tyr Leu Ser  
35 40 45  
Arg Gly Phe Phe Ser Arg Glu Pro Ile Cys Pro Phe Glu Glu Lys  
50 55 60  
Thr Lys Val Glu Arg Met Val Glu Asp Tyr Leu Ala Ser Gly Tyr  
65 70 75  
Gln Asp Ser Val Thr Phe Asp Asp Val Ala Val Asp Phe Thr Pro  
80 85 90  
Glu Glu Trp Ala Leu Leu Asp Thr Thr Glu Lys Tyr Leu Tyr Arg  
95 100 105  
Asp Val Met Leu Glu Asn Tyr Met Asn Leu Ala Ser Val Glu Trp  
110 115 120  
Glu Ile Gln Pro Arg Thr Lys Arg Ser Ser Leu Gln Gln Gly Phe  
125 130 135  
Leu Lys Asn Gln Ile Phe Ser Gly Ile Gln Met Thr Arg Gly Tyr  
140 145 150  
Ser Gly Trp Lys Leu Cys Asp Cys Lys Asn Cys Gly Glu Val Phe

Arg	Glu	Gln	Phe	155	Cys	Leu	Lys	Thr	His	160	Met	Arg	Val	Gln	Asn	165	Gly
				170						175							180
Gly	Asn	Thr	Ser	185	Glu	Gly	Asn	Cys	Tyr	190	Gly	Lys	Asp	Thr	Leu		195
Val	His	Lys	Glu	200	Ala	Ser	Thr	Gly	Gln	205	Glu	Leu	Ser	Lys	Phe		210
Pro	Cys	Gly	Lys	215	Val	Phe	Thr	Leu	Thr	220	Pro	Gly	Leu	Ala	Val		225
Leu	Glu	Val	Leu	230	Asn	Ala	Arg	Gln	Pro	235	Tyr	Lys	Cys	Lys	Glu		240
Gly	Lys	Gly	Phe	245	Lys	Tyr	Phe	Ala	Ser	250	Leu	Asp	Asn	His	Met		255
Ile	His	Thr	Asp	260	Glu	Lys	Leu	Cys	Glu	265	Phe	Gln	Glu	Tyr	Gly		270
Ala	Val	Thr	Ala	275	Ser	Ser	His	Leu	Lys	280	Gln	Cys	Val	Ala	Val		285
Thr	Gly	Lys	Lys	290	Ser	Lys	Lys	Thr	Lys	295	Lys	Cys	Gly	Lys	Ser		300
Thr	Asn	Phe	Ser	305	Gln	Leu	Tyr	Ala	Pro	310	Val	Lys	Thr	His	Lys		315
Glu	Lys	Ser	Phe	320	Glu	Cys	Lys	Glu	Cys	325	Gly	Arg	Ser	Phe	Arg		330
Ser	Ser	Cys	Leu	335	Asn	Asp	His	Ile	Gln	340	Ile	His	Thr	Gly	Ile		345
Pro	His	Lys	Cys	350	Thr	Tyr	Cys	Gly	Lys	355	Ala	Phe	Thr	Arg	Ser		360
Gln	Leu	Thr	Glu	365	His	Val	Arg	Thr	His	370	Thr	Gly	Ile	Lys	Pro		375
Glu	Cys	Lys	Glu	380	Cys	Gly	Gln	Ala	Phe	385	Ala	Gln	Tyr	Ser	Gly		390
Ser	Ile	His	Ile	395	Arg	Ser	His	Ser	Gly	400	Lys	Lys	Pro	Tyr	Gln		405
Lys	Glu	Cys	Gly	410	Lys	Ala	Phe	Thr	Thr	415	Ser	Thr	Ser	Leu	Ile		420
His	Thr	Arg	Ile	425	His	Thr	Gly	Glu	Lys	430	Pro	Tyr	Glu	Cys	Val		435
Cys	Gly	Lys	Thr	440	Phe	Ile	Thr	Ser	Ser	445	Arg	Arg	Ser	Lys	His		450
Lys	Thr	His	Ser	455	Gly	Glu	Lys	Pro	Phe	460	Val	Cys	Lys	Ile	Cys		465
Lys	Ala	Phe	Leu	470	Tyr	Ser	Ser	Arg	Leu	475	Asn	Val	His	Leu	Arg		480
His	Thr	Gly	Glu	485	Lys	Pro	Phe	Val	Cys	490	Lys	Glu	Cys	Gly	Lys		495
Phe	Ala	Val	Ser	500	Ser	Arg	Leu	Ser	Arg	505	His	Glu	Arg	Ile	His		510
Gly	Glu	Lys	Pro	515	Tyr	Glu	Cys	Lys	Asp	520	Met	Ser	Val	Thr	Ile		

&lt;210&gt; 125

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1090358.10.orf1:2002JAN18

&lt;400&gt; 125

Asn	Ser	Tyr	Leu	Leu	Leu	Arg	His	Ser	Phe	Asn	Cys	Gly	Leu	Phe
1				5					10					15
Val	Val	Val	Val	Phe	Gln	Gly	Arg	Ser	Pro	Arg	Lys	Ile	Asp	Gln

	20		25		30
Phe Cys Asn Ser Ser	Asn Met Val His Gly	Ser Val Thr Phe Arg			
	35		40		45
Asp Val Ala Ile Asp	Phe Ser Gln Glu Glu	Trp Glu Cys Leu Gln			
	50		55		60
Pro Asp Gln Arg Thr	Leu Tyr Arg Asp Val	Met Leu Glu Asn Tyr			
	65		70		75
Ser His Leu Ile Ser	Leu Gly Ser Ser Ile	Ser Lys Pro Asp Val			
	80		85		90
Ile Thr Leu Leu Glu	Gln Glu Lys Glu Pro	Trp Met Val Val Arg			
	95		100		105
Lys Glu Thr Ser Arg	Arg Tyr Pro Asp Leu	Glu Leu Lys Tyr Gly			
	110		115		120
Pro Glu Lys Val Ser	Pro Glu Asn Asp Thr	Ser Glu Val Asn Leu			
	125		130		135
Pro Lys Gln Val Ile	Lys Gln Ile Ser Thr	Thr Leu Gly Ile Glu			
	140		145		150
Ala Phe Tyr Phe Arg	Asn Asp Ser Glu Tyr	Arg Gln Phe Glu Gly			
	155		160		165
Leu Gln Gly Tyr Gln	Glu Gly Asn Ile Asn	Gln Lys Met Ile Ser			
	170		175		180
Tyr Glu Lys Leu Pro	Thr His Thr Pro His	Ala Ser Leu Ile Cys			
	185		190		195
Asn Thr His Lys Pro	Tyr Glu Cys Lys Glu	Cys Gly Lys Tyr Phe			
	200		205		210
Ser Arg Ser Ala Asn	Leu Ile Gln His Gln	Ser Ile His Thr Gly			
	215		220		225
Glu Lys Pro Phe Glu	Cys Lys Glu Cys Gly	Lys Ala Phe Arg Leu			
	230		235		240
His Ile Gln Phe Thr	Arg His Gln Lys Phe	His Thr Gly Glu Lys			
	245		250		255
Pro Leu Asn Val Thr	Asn Val Glu Arg Pro	Leu Val Phe Leu Pro			
	260		265		270
Cys Leu Ile Ala Ile	Arg Thr Phe Thr Gln	Val Arg Asn Cys Leu			
	275		280		285
Asn Val Arg Asn Val	Gly Ser Pro Leu Ile	Val Ala Gln Thr Leu			
	290		295		300
Phe Asn Ile Arg Val	Phe Ile Leu Val				
	305				

&lt;210&gt; 126

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1097492.2.orf2:2002JAN18

&lt;400&gt; 126

Ala Arg Phe Pro Gly	Ser Thr Gly Tyr Ile	Trp Pro Lys Ser Asp			
1	5	10			15
Ser Leu Gly Ala Leu	Val His Ser Pro Val	Asn Cys Pro Leu Leu			
	20	25			30
Gly Phe Ser Ala Val	Ser Thr Ser Leu Pro	Gln Gly Tyr Leu Trp			
	35	40			45
Val Gly Gly Gly Gln	Glu Gly Ala Gly Gln	Val Glu Ile Phe			
	50	55			60
Ser Leu Asn Arg Pro	Ser Pro Arg Thr Val	Lys Ser Phe Pro Leu			
	65	70			75
Ala Ala Pro Val Leu	Cys Met Glu Tyr Ile	Pro Glu Leu Glu Glu			
	80	85			90
Glu Ala Glu Ser Arg	Asp Glu Ser Pro Thr	Val Ala Asp Pro Ser			



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          95          100          105
Ala Thr Val His Pro Thr Ile Cys Leu Gly Leu Gln Asp Gly Ser
          110          115          120
Ile Leu Leu Tyr Ser Ser Val Asp Thr Gly Thr Gln Cys Leu Val
          125          130          135
Ser Cys Arg Ser Pro Gly Leu Gln Pro Val Leu Cys Leu Arg His
          140          145          150
Ser Pro Phe His Leu Leu Ala Gly Leu Gln Asp Gly Thr Leu Ala
          155          160          165
Ala Tyr Pro Arg Thr Ser Gly Gly Val Leu Trp Asp Leu Glu Ser
          170          175          180
Pro Pro Val Cys Leu Thr Val Gly Pro Gly Pro Val Arg Thr Leu
          185          190          195
Leu Ser Leu Glu Asp Ala Val Trp Ala Ser Cys Gly Pro Arg Val
          200          205          210
Thr Val Leu Glu Ala Thr Thr Leu Gln Pro Gln Gln Ser Phe Glu
          215          220          225
Ala His Gln Asp Glu Ala Val Ser Val Thr His Met Val Lys Ala
          230          235          240
Gly Ser Gly Val Trp Met Ala Phe Ser Ser Gly Thr Ser Ile Arg
          245          250          255
Leu Phe His Thr Glu Thr Leu Glu His Leu Gln Glu Ile Asn Ile
          260          265          270
Ala Thr Arg Thr Thr Phe Leu Leu Pro Gly Gln Lys His Leu Cys
          275          280          285
Val Thr Ser Leu Leu Ile Cys Gln Gly Leu Leu Trp Val Gly Thr
          290          295          300
Asp Gln Gly Val Ile Val Leu Leu Pro Val Pro Arg Leu Glu Gly
          305          310          315
Ile Pro Lys Ile Thr Gln Trp Ala Leu Trp Ala Cys Gly Leu Pro
          320          325          330
Gly Cys Gly Tyr Gln His Pro Gly Pro
          335

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<210> 127  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:1099945.26.orf2:2002JAN18

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<400> 127
Glu Ala Arg Pro Ile Leu Ser Leu Ser His Thr Leu Thr His Leu
  1      5      10
Thr Cys Trp Leu Val Thr Ser Lys Asp Thr Pro Ile Cys Leu Ala
      20      25      30
Pro Trp Leu Ala Ala Ala Pro Thr His Pro Cys Pro Pro Pro Ala
      35      40      45
Gln Ala Pro Asp Pro Lys Glu Glu Val Glu Gly Ala Cys Pro Pro
      50      55      60
Leu Ser Ala Met Gln His Leu Leu Glu Ala Ala Gln Ser Leu Leu
      65      70      75
Thr Ser Val Pro His Leu Ser His Arg Met Gln Lys Met Thr Ser
      80      85      90
Lys Ala Tyr His Leu Gln Lys Ser Thr Cys Gly Lys Cys Gly Tyr
      95      100      105
Pro Ala Lys Arg Lys Arg Lys Tyr Asn Trp Ser Ala Lys Ala Lys
      110      115      120
Arg Arg Asn Thr Thr Gly Thr Gly Arg Met Arg His Leu Lys Ile
      125      130      135
Val Tyr Arg Arg Phe Arg His Gly Phe Arg Glu Gly Thr Thr Pro

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122/218

140  
 Lys Pro Lys Arg Ala Ala Val Ala Ala 145 150  
 155 160

<210> 128  
 <211> 352  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:110016.1.orf1:2002JAN18

<400> 128  
 Pro Ser Arg Ser Ala Arg Ala Ser Cys Thr Trp Arg Arg Cys Pro  
 1 5 10 15  
 Arg Thr Trp Trp Pro Arg Cys Cys Thr Thr Cys Thr His Gln Arg  
 20 25 30  
 Ser Arg Trp Met Arg Arg Ala Cys Arg Ile Cys Ser Pro Arg His  
 35 40 45  
 Thr Ala Ser Arg Ser Leu Pro Ser Ser Pro Ser Ala Cys Pro Ser  
 50 55 60  
 Cys Arg Ser Ala Cys Ala Ser Pro Thr Ala Trp Pro Ser Ser Val  
 65 70 75  
 Ser Ala Ser Cys Ser Thr Ala Arg Val Ser Pro Trp Leu Pro Ala  
 80 85 90  
 Thr Ser Ser Ala Leu Thr Ser Arg Trp Trp Arg Ala Thr Leu Thr  
 95 100 105  
 Ser Ser Asp Ser Arg Arg Arg Ala His Arg His His Leu Gln Arg  
 110 115 120  
 Arg Ala Leu Thr Trp Arg Arg Arg Ser Leu Val Phe Glu Ala Val  
 125 130 135  
 Met Arg Trp Ala Gly Ser Gly Asp Ala Glu Ala Gln Ala Glu Arg  
 140 145 150  
 Gln Arg Ala Leu Pro Thr Val Phe Glu Ser Val Arg Cys Arg Leu  
 155 160 165  
 Leu Pro Arg Ala Phe Leu Glu Ser Arg Val Glu Arg His Pro Leu  
 170 175 180  
 Val Arg Ala Gln Pro Glu Leu Leu Arg Lys Val Gln Met Val Lys  
 185 190 195  
 Asp Ala His Glu Gly Arg Ile Thr Thr Leu Arg Lys Lys Lys Lys  
 200 205 210  
 Gly Lys Asp Gly Ala Gly Ala Lys Glu Ala Asp Lys Gly Thr Ser  
 215 220 225  
 Lys Ala Lys Ala Glu Glu Asp Glu Glu Ala Glu Arg Ile Leu Pro  
 230 235 240  
 Gly Ile Leu Asn Asp Thr Leu Arg Phe Gly Met Phe Leu Gln Asp  
 245 250 255  
 Leu Ile Phe Met Ile Ser Glu Glu Gly Ala Val Ala Tyr Asp Pro  
 260 265 270  
 Ala Ala Asn Glu Cys Tyr Cys Ala Ser Leu Ser Ser Gln Val Pro  
 275 280 285  
 Lys Asn His Val Ser Leu Val Thr Lys Glu Asn Gln Val Phe Val  
 290 295 300  
 Ala Gly Gly Leu Phe Tyr Asn Glu Asp Asn Lys Glu Asp Pro Met  
 305 310 315  
 Ser Ala Tyr Phe Leu Gln Phe Asp His Leu Val Gly Gly Gln Arg  
 320 325 330  
 Asp Gln Gly Arg Arg Ala Leu Pro Gly Leu Gly His Val Leu Arg  
 335 340 345  
 Gln Ala Val Ile Gln Met Gly  
 350

<210> 129  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:1137613.10.orf2:2002JAN18

<220>  
 <221> unsure  
 <222> (1) ... (138)  
 <223> unknown or other

<400> 129  
 Arg Thr His Gln Leu Asn Asn Ile Pro His Val Ala Asp Thr Asn  
 1 5 10 15  
 Lys Ala Ala Val Ser Ser Phe Ser Lys Pro Leu Lys Gly Ser Ala  
 20 25 30  
 Gly Gly Arg Arg Asn Ser Lys Gly Gly Pro Arg Gln Gly Ala Ile  
 35 40 45  
 Gly Leu Gly Leu Arg Glu Pro Glu Thr Ala Ala Ala Ala Ala  
 50 55 60  
 Ala Ala Ala Gly Gly Ala Gln Gly Thr Pro Xaa Leu Pro Val Leu  
 65 70 75  
 Cys Leu Gly Pro Ser Leu Leu Pro Arg Ala Gln Cys Gly Leu Ala  
 80 85 90  
 Ser Val Lys Glu Phe Asp Lys Lys Tyr Asn Pro Thr Trp His Cys  
 95 100 105  
 Ile Val Gly Arg Asn Phe Gly Ser Tyr Val Thr His Glu Thr Lys  
 110 115 120  
 His Phe Ile Tyr Phe Tyr Leu Gly Gln Val Ala Ile Leu Leu Phe  
 125 130 135  
 Lys Ser Gly

<210> 130  
 <211> 608  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:118836.26.orf2:2002JAN18

<400> 130  
 Gly Arg Leu Ser Ser Gln Pro Trp Met Phe Ser Ser Cys Gly Arg  
 1 5 10 15  
 Pro Ala Ser Lys Ser Thr Thr Ser Ser Thr Pro Arg Thr Arg Gln  
 20 25 30  
 Leu His Ala Trp Ser Arg Cys Trp Asn Gly Ala Phe Thr Pro Cys  
 35 40 45  
 Arg Leu Ser Ala Ser Pro Ala Thr Asn Ala Thr Arg Trp Gly Met  
 50 55 60  
 Ala Ala Pro Arg Cys Trp Ser Arg Pro Cys Arg Glu Thr Leu Ser  
 65 70 75  
 Trp Ser Trp Arg Ala Ala Pro Trp Pro Leu Ser Pro Thr Gly Thr  
 80 85 90  
 Ala Ser Trp Lys Pro Val Cys Leu Phe Pro Arg Pro Pro Gly Lys  
 95 100 105  
 Thr Ala Pro Ala Arg Ala Val Pro Ser Arg Met Cys Ser Arg Pro  
 110 115 120  
 Thr Met Gln Pro Ser Lys Ser Met Ala Pro Pro Pro Arg Arg Ala

Leu Pro Leu Pro	125	Val Val Ala Ser Ala	130	Glu Pro Val Arg Ser	135
	140		145		150
Ser Pro Ala Arg	155	Cys Gln Ala Trp Leu	160	Arg Ala Thr Arg His	165
	170		175		180
Ala Ser Pro Arg	185	Ser Leu Gln Ser Gly	190	Gly Ala Arg Ser Gly	195
	200		205		210
Thr Thr Pro Cys	215	Thr Ala Leu Thr Pro	220	Ser Thr Ala Phe Pro	225
	230		235		240
Val Ala Leu Pro	245	His Leu Phe His Ala	250	Ser Tyr Trp Glu Ser	255
	260		265		270
Asp Val Val Ser	275	Phe Leu Leu Arg Gln	280	Val Met Arg His Asp	285
	290		295		300
Ser Ser Ile Leu	305	Glu Leu Asp Gly Lys	310	Glu Val Ser Val Phe	315
	320		325		330
Pro Ser Lys Pro	335	Arg Glu Lys Trp Gln	340	Arg Lys Arg Thr His	345
	350		355		360
Lys Leu Arg Asn	365	Val Thr Ala Asn His	370	Arg Ile Asn Asp Ala	375
	380		385		390
Ala Asn Glu Asp	395	Gly Pro Gln Val Leu	400	Thr Gly Arg Phe Met	405
	410		415		420
Gly Pro Leu Asp	425	Met Val Thr Leu Thr	430	Gly Glu Lys Val Asp	435
	440		445		450
His Ile Met Thr	455	Gln Pro Pro Ser Gly	460	Glu Trp Leu Tyr Leu	465
	470		475		480
Thr Leu Val Thr	485	Asn Asn Ser Gly Arg	490	Val Ser Tyr Thr Ile	495
	500		505		510
Glu Ser His Arg	515	Leu Gly Val Gly Val	520	Tyr Pro Ile Lys Met	525
	530		535		540
Val Arg Gly Asp	545	His Thr Phe Ala Asp	550	Ser Tyr Ile Thr Val	555
	560		565		570
Pro Lys Gly Thr	575	Glu Phe Val Val Phe	580	Ser Ile Asp Gly Ser	585
	590		595		600
Ala Ala Ser Val		Ser Ile Met Gly Ser		Asp Pro Lys Val Arg	
Gly Ala Val Asp		Val Val Arg His Trp		Gln Asp Leu Gly Tyr	
Ile Ile Tyr Val		Thr Gly Arg Pro Asp		Met Gln Lys Gln Arg	
Val Ala Trp Leu		Ala Gln His Asn Phe		Pro His Gly Val Val	
Phe Cys Asp Gly		Leu Val His Asp Pro		Leu Arg His Lys Ala	
Phe Leu Lys Leu		Leu Ile Ser Glu Leu		His Leu Arg Val His	
Ala Tyr Gly Ser		Thr Lys Asp Val Ala		Val Tyr Ser Ala Ile	
Leu Ser Pro Met		Gln Ile Tyr Ile Val		Gly Arg Pro Thr Lys	
Leu Gln Gln Gln		Cys Gln Phe Ile Thr		Asp Gly Tyr Ala Ala	
Leu Ala Gln Leu		Lys Tyr Ser His Arg		Ala Arg Pro Ala Arg	
Thr Ala Thr Arg		Met Ala Leu Arg Lys		Gly Ser Phe Gly Leu	
Gly Gln Gly Asp		Phe Leu Arg Ser Arg		Asn His Leu Leu Arg	
Ile Ser Ala Gln		Pro Ser Gly Pro Ser		His Arg His Glu Arg	
Gln Ser Gln Ala		Asp Gly Glu Gln Arg		Gly Gln Arg Ser Met	
Val Ala Ala Gly		Cys Trp Gly Arg Ala		Met Thr Gly Arg Leu	

Pro Gly Ala Ala Ala Gly Pro Lys  
605

<210> 131

<211> 694

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Incyte ID No: LG:1330261.32.orf1:2002JAN18

<400> 131

Asp	Gly	Ala	Leu	Pro	Ser	Phe	Leu	His	Pro	Gln	Tyr	Phe	Lys	Tyr
1				5					10					15
Glu	Phe	Pro	Glu	Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser
				20					25					30
Asn	Lys	Ala	Phe	Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu
				35					40					45
Cys	Pro	Val	Tyr	Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met
				50					55					60
Tyr	Gln	Thr	Met	Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys
				65					70					75
Asp	Phe	Pro	Ser	Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr
				80					85					90
Glu	Asp	Gln	Ala	Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala
				95					100					105
Glu	Asp	Glu	Pro	Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser
				110					115					120
Val	Leu	Val	Ser	Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly
				125					130					135
Met	Leu	Phe	Cys	Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr
				140					145					150
Val	Leu	Leu	Ala	Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr
				155					160					165
Leu	Leu	Val	Ala	Ile	Asp	Arg	Ala	Cys	Pro	Glu	Ser	Gly	His	Pro
				170					175					180
Arg	Val	Leu	Ala	Asp	Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly
				185					190					195
Tyr	Asn	Tyr	Gly	Ser	Phe	Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly
				200					205					210
Leu	Val	Asp	Ser	Ala	Gly	Thr	Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln
				215					220					225
Gly	His	Asp	Gln	Phe	Lys	Arg	Arg	Leu	Pro	Ser	Gly	Gln	Met	Arg
				230					235					240
Gln	Leu	Cys	Ile	Ala	Met	Gly	Arg	Ser	Phe	Glu	Pro	Val	Gly	Thr
				245					250					255
Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val	Glu	Glu	Asp	Asp	Tyr
				260					265					270
Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys	Asn	Val	Ile	Arg	Thr
				275					280					285
Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala	Arg	Lys	Asp	Lys	Arg
				290					295					300
Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe	Trp	Asn	Ile	Ala	Thr
				305					310					315
Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val	Gln	Leu	Val	Ile	Thr
				320					325					330
Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn	Gln	Asp	Ile	Cys	Tyr
				335					340					345
Tyr	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly	Asn	Leu	Ser	Ala	Phe
				350					355					360
Asn	Asn	Ile	Leu	Ser	Asn	Leu	Gly	Tyr	Ile	Leu	Leu	Gly	Leu	Leu
				365					370					375

Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile	Asn	His	Asn	Arg	Ala	
				380					385					390	
Leu	Leu	Arg	Asn	Asp	Leu	Cys	Ala	Leu	Glu	Cys	Gly	Ile	Pro	Lys	
				395					400					405	
His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr	Ala	Leu	Met	Met	Glu	
				410					415					420	
Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys	Pro	Asn	Tyr	Thr	Asn	
				425					430					435	
Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met	Ile	Ala	Gly	Leu	Cys	
				440					445					450	
Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro	Asp	Ile	Asn	Ala	Ser	
				455					460					465	
Ala	Tyr	Ser	Ala	Tyr	Ala	Cys	Leu	Ala	Ile	Val	Ile	Phe	Phe	Ser	
				470					475					480	
Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	Thr	Ala	Phe	Trp	Ile	
				485					490					495	
Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	Leu	Leu	Leu	Ser	Thr	
				500					505					510	
Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	Asp	Ser	Gly	Ile	Phe	
				515					520					525	
Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	Cys	Ile	Arg	Gln	Cys	
				530					535					540	
Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	Leu	Leu	Val	Met	Gly	
				545					550					555	
Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	Gly	Leu	Ile	Met	Arg	
				560					565					570	
Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	Ile	Gly	Ile	Cys	Asn	
				575					580					585	
Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	Met	Lys	Leu	Arg	Ser	
				590					595					600	
Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	Cys	Ile	Val	Cys	Thr	
				605					610					615	
Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	Phe	Phe	Gln	Gly	Leu	
				620					625					630	
Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	Arg	Glu	His	Asn	Arg	
				635					640					645	
Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	His	Asp	Ile	Trp	His	
				650					655					660	
Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	Phe	Leu	Val	Ser	Gly	
				665					670					675	
Pro	Pro	Gly	Arg	Ala	Gly	Trp	Val	Arg	Glu	Gly	Ser	Ser	Cys	Leu	
				680					685					690	
Leu	Leu	Cys	Gly												

&lt;210&gt; 132

&lt;211&gt; 401

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1347461.28.orf3:2002JAN18

&lt;400&gt; 132

Phe	Ile	Trp	His	Lys	Ser	Ile	Leu	Ser	Arg	Met	Ala	Glu	Ala	Val	
1				5					10					15	
Leu	Ile	Asp	Leu	Phe	Gly	Leu	Lys	Leu	Asn	Ser	Gln	Lys	Asn	Cys	
				20					25					30	
His	Gln	Thr	Leu	Leu	Lys	Thr	Leu	Asn	Ala	Val	Gln	Tyr	His	His	
				35					40					45	
Ala	Ala	Lys	Ala	Lys	Phe	Leu	Cys	Ile	Met	Cys	Cys	Ser	Asn	Ile	
				50					55					60	

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Ser Tyr Glu Arg Asp Gly Glu Gln Asp Asn Cys Glu Ile Glu Thr
65 70 75
Ser Asn Gly Leu Ser Ala Leu Leu Glu Glu Phe Glu Ile Val Ser
80 85 90
Cys Pro Ser Met Ala Ala Thr Leu Tyr Thr Ile Lys Gln Lys Ile
95 100 105
Asp Glu Lys Asn Leu Ser Ser Ile Lys Val Ile Val Pro Arg His
110 115 120
Arg Lys Thr Leu Met Lys Ala Phe Ile Asp Gln Leu Phe Thr Asp
125 130 135
Val Tyr Asn Phe Glu Phe Glu Asp Leu Gln Val Thr Phe Arg Gly
140 145 150
Gly Leu Phe Lys Gln Ser Ile Glu Ile Asn Val Ile Thr Ala Gln
155 160 165
Glu Leu Arg Gly Ile Gln Asn Glu Ile Glu Thr Phe Leu Arg Ser
170 175 180
Leu Pro Ala Leu Arg Gly Lys Leu Thr Ile Ile Thr Ser Ser Leu
185 190 195
Ile Pro Asp Ile Phe Ile His Gly Phe Thr Thr Arg Thr Gly Gly
200 205 210
Ile Ser Tyr Ile Pro Thr Leu Ser Ser Phe Asn Leu Phe Ser Ser
215 220 225
Ser Lys Arg Arg Asp Pro Lys Val Val Val Gln Gly Ile Lys Thr
230 235 240
His His Ser Asn Asp Ile Trp Ile Met Gly Arg Lys Glu Pro Asp
245 250 255
Ser Tyr Asp Gly Ile Thr Thr Asn Gln Arg Gly Val Thr Ile Ala
260 265 270
Ala Leu Gly Ala Asp Cys Ile Pro Ile Val Phe Ala Asp Pro Val
275 280 285
Lys Lys Ala Cys Gly Val Ala His Ala Gly Trp Lys Gly Thr Leu
290 295 300
Leu Gly Val Ala Met Ala Thr Val Asn Ala Met Ile Ala Glu Tyr
305 310 315
Gly Cys Ser Leu Glu Asp Ile Val Val Val Leu Gly Pro Ser Val
320 325 330
Gly Pro Cys Cys Phe Thr Leu Pro Arg Glu Ser Ala Glu Ala Phe
335 340 345
His Asn Leu His Pro Ala Cys Val Gln Leu Phe Asp Ser Pro Asn
350 355 360
Pro Cys Ile Asp Ile Arg Lys Ala Thr Ser Phe Pro Lys Asp Ser
365 370 375
Ser Arg Thr Gly Arg Asn Ser Ser Thr Glu Tyr Ser Gly Pro Glu
380 385 390
Pro Arg Ser Gln Pro Leu Tyr Ile Leu Pro Ser
395 400

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&lt;210&gt; 133

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1383494.16.orf3:2002JAN18

&lt;400&gt; 133

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Ser Gln His Phe Pro Arg Pro Ser Val Glu Thr Glu Val Gly Asp
1 5 10 15
Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys
20 25 30
Val Ile Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala
35 40 45

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Gln	Glu	Gln	Glu	Asp	Trp	Lys	Lys	Tyr	Ile	Thr	Gly	Thr	Asp	Ile	
				50					55					60	
Leu	Asp	Met	Lys	Leu	Glu	Asp	Ile	Leu	Glu	Ser	Ile	Asn	Ser	Ile	
				65					70					75	
Lys	Ser	Arg	Leu	Ser	Lys	Ser	Gly	His	Ile	Gln	Thr	Leu	Leu	Arg	
				80					85					90	
Ala	Phe	Glu	Ala	Arg	Asp	Arg	Asn	Ile	Gln	Glu	Ser	Asn	Phe	Asp	
				95					100					105	
Arg	Val	Asn	Phe	Trp	Ser	Met	Val	Asn	Leu	Val	Val	Met	Val	Val	
				110					115					120	
Val	Ser	Ala	Ile	Gln	Val	Tyr	Met	Leu	Lys	Ser	Leu	Phe	Glu	Asp	
				125					130					135	
Lys	Arg	Lys	Ser	Arg	Thr										
				140											

&lt;210&gt; 134

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1400155.1.orf2:2002JAN18

&lt;400&gt; 134

Ala	Trp	Ala	Ala	Val	Ile	Thr	Pro	Trp	Asn	Phe	Pro	Ser	Ala	Met	
1				5					10					15	
Ile	Thr	Arg	Lys	Val	Gly	Ala	Ala	Leu	Ala	Ala	Gly	Cys	Thr	Val	
				20					25					30	
Val	Val	Lys	Pro	Ala	Glu	Asp	Thr	Pro	Phe	Ser	Ala	Leu	Ala	Leu	
				35					40					45	
Ala	Glu	Leu	Ala	Ser	Gln	Ala	Gly	Ile	Pro	Ser	Gly	Val	Tyr	Asn	
				50					55					60	
Val	Ile	Pro	Cys	Ser	Arg	Lys	Asn	Ala	Lys	Glu	Val	Gly	Glu	Ala	
				65					70					75	
Ile	Cys	Thr	Asp	Pro	Leu	Val	Ser	Lys	Ile	Ser	Phe	Thr	Gly	Ser	
				80					85					90	
Thr	Thr	Thr	Gly	Lys	Ile	Leu	Leu	His	His	Ala	Ala	Asn	Ser	Val	
				95					100					105	
Lys	Arg	Val	Ser	Met	Glu	Leu	Gly	Gly	Leu	Ala	Pro	Phe	Ile	Val	
				110					115					120	
Phe	Asp	Ser	Ala	Asn	Val	Asp	Gln	Ala	Val	Ala	Gly	Ala	Met	Ala	
				125					130					135	
Ser	Lys	Phe	Arg	Asn	Thr	Gly	Gln	Thr	Cys	Val	Cys	Ser	Asn	Gln	
				140					145					150	
Phe	Leu	Val	Gln	Arg	Gly	Ile	His	Asp	Ala	Phe	Val	Lys	Ala	Phe	
				155					160					165	
Ala	Glu	Ala	Met	Lys	Lys	Asn	Leu	Arg	Val	Gly	Asn	Gly	Phe	Glu	
				170					175					180	
Glu	Gly	Thr	Thr	Gln	Gly	Pro	Leu	Ile	Asn	Glu	Lys	Ala	Val	Glu	
				185					190					195	
Lys	Val	Glu	Lys	Gln	Val	Asn	Asp	Ala	Val	Ser	Lys	Gly	Ala	Thr	
				200					205					210	
Val	Val	Thr	Gly	Gly	Lys	Arg	His	Gln	Leu	Gly	Lys	Asn	Phe	Phe	
				215					220					225	
Glu	Pro	Thr	Leu	Leu	Cys	Asn	Val	Thr	Gln	Asp	Met	Leu	Cys	Thr	
				230					235					240	
His	Glu	Glu	Thr	Phe	Gly	Pro	Leu	Ala	Pro	Val	Ile	Lys	Phe	Asp	
				245					250					255	
Thr	Glu	Glu	Glu	Ala	Ile	Ala	Ile	Ala	Asn	Ala	Ala	Asp	Val	Gly	
				260					265					270	
Leu	Ala	Gly	Tyr	Phe	Tyr	Ser	Gln	Asp	Pro	Ala	Gln	Ile	Trp	Arg	
				275					280					285	



WO 03/062379

Val Ala Glu Gln Leu Glu Val Gly Met Val Gly Val Asn Glu Gly  
 290 295 300  
 Leu Ile Ser Ser Val Glu Cys Pro Phe Gly Gly Val Lys Gln Ser  
 305 310 315  
 Gly Leu Gly Arg Glu Gly Ser Lys Tyr Gly Ile Asp Glu Tyr Leu  
 320 325 330  
 Glu Leu Lys Tyr Val Cys Tyr Gly Gly Leu  
 335 340

&lt;210&gt; 135

&lt;211&gt; 229

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1446621.1.orf3:2002JAN18

&lt;400&gt; 135

Lys Leu Asp Tyr Arg Arg Glu Pro Pro Arg Pro Val Tyr Val Leu  
 1 5 10 15  
 Trp Ile Cys Glu Tyr Ser Tyr Ser Val Leu Phe Ile Asn Thr Tyr  
 20 25 30  
 Asp Leu Thr Gln Lys Val Lys Val Asn Thr Leu Trp Gly Gly Pro  
 35 40 45  
 Val Ser Val Gln Gly Gly Ser Pro Ala Arg Lys Gly Cys Ser Leu  
 50 55 60  
 Arg Cys His Ser Ser Phe Ser Pro Ala Ser Asp His Ile Cys His  
 65 70 75  
 Ser Gly Pro Glu Gly Ala Gly Gly Pro Ser Asn Gln Ala Arg Ser  
 80 85 90  
 Trp Ser Arg Gln Gly Gly Phe Arg Gly Phe Gly Ala Ala Phe Val  
 95 100 105  
 Ser Arg Cys Arg Gln Lys Leu Gln Phe Ser Ser Val Cys Phe Val  
 110 115 120  
 Ser Ser Ala Arg Arg Ser Pro Ala Cys Val Ala Leu Arg Pro Ala  
 125 130 135  
 Gly Ile Gly Arg Ser Thr Ala Lys Thr Pro Gly Pro Pro Gly Ser  
 140 145 150  
 Leu Glu Met Gly Ala Leu Thr Phe Arg Asp Val Ala Ile Glu Phe  
 155 160 165  
 Ser Leu Glu Glu Trp Gln Cys Leu Asp Thr Glu Gln Gln Asn Leu  
 170 175 180  
 Tyr Arg Asn Val Met Leu Asp Asn Tyr Arg Asn Leu Val Phe Leu  
 185 190 195  
 Gly Ile Ala Val Ser Lys Pro Asp Leu Ile Thr Cys Leu Glu Gln  
 200 205 210  
 Glu Lys Glu Pro Trp Asn Leu Lys Thr His Asp Met Val Ala Lys  
 215 220 225  
 Pro Pro Gly Arg

&lt;210&gt; 136

&lt;211&gt; 407

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:144920.1.orf1:2002JAN18

&lt;400&gt; 136

Val Leu Leu Asp Glu Ala Gln Arg Leu Leu Tyr Arg Asp Val Met

1	5	10	15
Leu Glu Asn Phe Ala	Leu Met Ala Ser	Leu Gly Cys Trp His	Gly
20	25	30	
Met Glu Asp Glu Glu	Ile Pro Phe Glu	Gln Ser Phe Ser Ile	Gly
35	40	45	
Met Ser Gln Ile Arg	Ile Pro Lys Gly	Gly Pro Ser Thr Gln	Lys
50	55	60	
Ala Tyr Pro Cys Gly	Thr Cys Gly Leu	Val Leu Lys Asp Ile	Leu
65	70	75	
His Leu Ala Glu His	Gln Glu Thr His	Pro Gly Gln Lys Pro	Tyr
80	85	90	
Met Cys Val Leu Cys	Gly Lys Gln Phe	Trp Phe Ser Ala Asn	Leu
95	100	105	
His Gln His Gln Lys	Gln His Ser Gly	Glu Lys Pro Phe Arg	Ser
110	115	120	
Asp Lys Ser Arg Pro	Phe Leu Leu Asn	Asn Cys Ala Val Gln	Ser
125	130	135	
Leu Glu Met Ser Phe	Val Thr Gly Glu	Ala Cys Lys Asp Phe	Leu
140	145	150	
Ala Ser Ser Ser Ile	Phe Glu His His	Ala Pro His Asn Glu	Trp
155	160	165	
Lys Pro His Ser Asn	Thr Lys Cys Glu	Glu Ala Ser His Cys	Gly
170	175	180	
Lys Arg His Tyr Lys	Cys Ser Glu Cys	Gly Lys Thr Phe Ser	Arg
185	190	195	
Lys Asp Ser Leu Val	Gln His Gln Arg	Val His Thr Gly Glu	Arg
200	205	210	
Pro Tyr Glu Cys Gly	Glu Cys Gly Lys	Thr Phe Ser Arg Lys	Pro
215	220	225	
Ile Leu Ala Gln His	Gln Arg Ile His	Thr Gly Glu Met Pro	Tyr
230	235	240	
Glu Cys Gly Ile Cys	Gly Lys Val Phe	Asn His Ser Ser Asn	Leu
245	250	255	
Ile Val His Gln Arg	Val His Thr Gly	Ala Arg Pro Tyr Lys	Cys
260	265	270	
Ser Glu Cys Gly Lys	Ala Tyr Ser His	Lys Ser Thr Leu Val	Gln
275	280	285	
His Glu Ser Ile His	Thr Gly Glu Arg	Pro Tyr Glu Cys Ser	Glu
290	295	300	
Cys Gly Lys Tyr Phe	Gly His Lys Tyr	Arg Leu Ile Lys His	Trp
305	310	315	
Ser Val His Thr Gly	Ala Arg Pro Tyr	Glu Cys Ile Ala Cys	Gly
320	325	330	
Lys Phe Phe Ser Gln	Ser Ser Asp Leu	Ile Ala His Gln Arg	Val
335	340	345	
His Asn Gly Glu Lys	Pro Tyr Val Cys	Ser Glu Cys Gly Lys	Ala
350	355	360	
Phe Ser His Lys His	Val Leu Val Gln	His His Arg Ile His	Thr
365	370	375	
Gly Glu Arg Pro Tyr	Lys Cys Ser Glu	Cys Gly Lys Ala Phe	Arg
380	385	390	
Gln Arg Ala Ser Leu	Ile Arg His Trp	Lys Ile His Thr Gly	Glu
395	400	405	
Arg Pro			

&lt;210&gt; 137

&lt;211&gt; 529

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1452619.1.orf2:2002JAN18

&lt;400&gt; 137

Arg	Gln	Gln	Leu	Arg	Gln	Arg	Gln	Ala	Gln	Val	Gln	Pro	Leu	Ala
1				5					10					15
Glu	His	Asn	Phe	Phe	Phe	Ser	Lys	Phe	Pro	Gly	Cys	Gly	Glu	Leu
				20					25					30
Ser	Leu	Gly	Glu	Val	Lys	Ser	Leu	Ser	Ser	Lys	Lys	Met	Asn	Gly
				35					40					45
Thr	Leu	Asp	His	Pro	Asp	Gln	Pro	Asp	Leu	Asp	Ala	Ile	Lys	Met
				50					55					60
Phe	Val	Gly	Gln	Val	Pro	Arg	Thr	Trp	Ser	Glu	Lys	Asp	Leu	Arg
				65					70					75
Glu	Leu	Phe	Glu	Gln	Tyr	Gly	Ala	Val	Tyr	Glu	Ile	Asn	Val	Leu
				80					85					90
Arg	Asp	Arg	Ser	Gln	Asn	Pro	Pro	Gln	Ser	Lys	Gly	Cys	Cys	Phe
				95					100					105
Val	Thr	Phe	Tyr	Thr	Arg	Lys	Ala	Ala	Leu	Glu	Ala	Gln	Asn	Ala
				110					115					120
Leu	His	Asn	Met	Lys	Val	Leu	Pro	Gly	Met	His	His	Pro	Ile	Gln
				125					130					135
Met	Lys	Pro	Ala	Asp	Ser	Glu	Lys	Asn	Asn	Ala	Val	Glu	Asp	Arg
				140					145					150
Lys	Leu	Phe	Ile	Gly	Met	Ile	Ser	Lys	Lys	Cys	Thr	Glu	Asn	Asp
				155					160					165
Ile	Arg	Val	Met	Phe	Ser	Ser	Phe	Gly	Gln	Ile	Glu	Glu	Cys	Arg
				170					175					180
Ile	Leu	Arg	Gly	Pro	Asp	Gly	Leu	Ser	Arg	Gly	Cys	Ala	Phe	Val
				185					190					195
Thr	Phe	Thr	Thr	Arg	Ala	Met	Ala	Gln	Thr	Ala	Ile	Lys	Ala	Met
				200					205					210
His	Gln	Ala	Gln	Thr	Met	Glu	Gly	Cys	Ser	Ser	Pro	Met	Val	Val
				215					220					225
Lys	Phe	Ala	Asp	Thr	Gln	Lys	Asp	Lys	Glu	Gln	Lys	Arg	Met	Ala
				230					235					240
Gln	Gln	Leu	Gln	Gln	Gln	Met	Gln	Gln	Ile	Ser	Ala	Ala	Ser	Val
				245					250					255
Trp	Gly	Asn	Leu	Ala	Gly	Leu	Asn	Thr	Leu	Gly	Pro	Gln	Tyr	Leu
				260					265					270
Ala	Leu	Tyr	Leu	Gln	Leu	Leu	Gln	Gln	Thr	Ala	Ser	Ser	Gly	Asn
				275					280					285
Leu	Asn	Thr	Leu	Ser	Ser	Leu	His	Pro	Met	Gly	Gly	Leu	Asn	Ala
				290					295					300
Met	Gln	Leu	Gln	Asn	Leu	Ala	Ala	Leu	Ala	Ala	Ala	Ala	Ser	Ala
				305					310					315
Ala	Gln	Asn	Thr	Pro	Ser	Gly	Thr	Asn	Ala	Leu	Thr	Thr	Ser	Ser
				320					325					330
Ser	Pro	Leu	Ser	Val	Leu	Thr	Ser	Ser	Ala	Gly	Ser	Ser	Pro	Ser
				335					340					345
Ser	Ser	Ser	Ser	Asn	Ser	Val	Asn	Pro	Ile	Ala	Ser	Leu	Gly	Ala
				350					355					360
Leu	Gln	Thr	Leu	Ala	Gly	Ala	Thr	Ala	Gly	Leu	Asn	Val	Gly	Ser
				365					370					375
Leu	Ala	Gly	Met	Ala	Ala	Leu	Asn	Gly	Gly	Leu	Gly	Ser	Ser	Gly
				380					385					390
Leu	Ser	Asn	Gly	Thr	Gly	Ser	Thr	Met	Glu	Ala	Leu	Thr	Gln	Ala
				395					400					405
Tyr	Ser	Gly	Ile	Gln	Gln	Tyr	Ala	Ala	Ala	Ala	Leu	Pro	Thr	Leu
				410					415					420
Tyr	Asn	Gln	Asn	Leu	Leu	Thr	Gln	Gln	Ser	Ile	Gly	Ala	Ala	Gly
				425					430					435
Ser	Gln	Lys	Glu	Gly	Pro	Glu	Gly	Ala	Asn	Leu	Phe	Ile	Tyr	His
				440					445					450

Leu	Pro	Gln	Glu	Phe	Gly	Asp	Gln	Asp	Leu	Leu	Gln	Met	Phe	Met
				455					460					465
Pro	Phe	Gly	Asn	Val	Val	Ser	Ala	Lys	Val	Phe	Ile	Asp	Lys	Gln
				470					475					480
Thr	Asn	Leu	Ser	Lys	Cys	Phe	Gly	Phe	Val	Ser	Tyr	Asp	Asn	Pro
				485					490					495
Val	Ser	Ala	Gln	Ala	Ala	Ile	Gln	Ser	Met	Asn	Gly	Phe	Gln	Ile
				500					505					510
Gly	Met	Lys	Arg	Leu	Lys	Val	Gln	Leu	Lys	Arg	Ser	Lys	Asn	Asp
				515					520					525
Ser	Lys	Pro	Tyr											

&lt;210&gt; 138

&lt;211&gt; 2245

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1453417.6.orf1:2002JAN18

&lt;400&gt; 138

Ala	Ala	Val	Cys	Val	Gly	Cys	Tyr	Arg	Leu	Arg	Trp	His	Ser	Ala
1				5					10					15
Gly	His	Gly	Thr	Asp	Cys	Gly	Glu	Cys	His	Arg	Arg	His	Thr	His
				20					25					30
Arg	Pro	Val	Phe	Gln	Ser	Ser	His	Tyr	Thr	Val	Asn	Val	Asn	Glu
				35					40					45
Asp	Arg	Pro	Ala	Gly	Thr	Thr	Val	Val	Leu	Ile	Ser	Ala	Thr	Asp
				50					55					60
Glu	Asp	Thr	Gly	Glu	Asn	Ala	Arg	Ile	Thr	Tyr	Phe	Met	Glu	Asp
				65					70					75
Ser	Ile	Pro	Gln	Phe	Arg	Ile	Asp	Ala	Asp	Thr	Gly	Ala	Val	Thr
				80					85					90
Thr	Gln	Ala	Glu	Leu	Asp	Tyr	Glu	Asp	Gln	Val	Ser	Tyr	Thr	Leu
				95					100					105
Ala	Ile	Thr	Ala	Arg	Asp	Asn	Gly	Ile	Pro	Gln	Lys	Ser	Asp	Thr
				110					115					120
Thr	Tyr	Leu	Glu	Ile	Leu	Val	Asn	Asp	Val	Asn	Asp	Asn	Ala	Pro
				125					130					135
Gln	Phe	Leu	Arg	Asp	Ser	Tyr	Gln	Gly	Ser	Val	Tyr	Glu	Asp	Val
				140					145					150
Pro	Pro	Phe	Thr	Ser	Val	Leu	Gln	Ile	Ser	Ala	Thr	Asp	Arg	Asp
				155					160					165
Ser	Gly	Leu	Asn	Gly	Arg	Val	Phe	Tyr	Thr	Phe	Gln	Gly	Gly	Asp
				170					175					180
Asp	Gly	Asp	Gly	Asp	Phe	Ile	Val	Glu	Ser	Thr	Ser	Gly	Ile	Val
				185					190					195
Arg	Thr	Leu	Arg	Arg	Leu	Asp	Arg	Glu	Asn	Val	Ala	Gln	Tyr	Val
				200					205					210
Leu	Arg	Ala	Tyr	Ala	Val	Asp	Lys	Gly	Met	Pro	Pro	Ala	Arg	Thr
				215					220					225
Pro	Met	Glu	Val	Thr	Val	Thr	Val	Leu	Asp	Val	Asn	Asp	Asn	Pro
				230					235					240
Pro	Val	Phe	Glu	Gln	Asp	Glu	Phe	Asp	Val	Phe	Val	Glu	Glu	Asn
				245					250					255
Ser	Pro	Ile	Gly	Leu	Ala	Val	Ala	Arg	Val	Thr	Ala	Thr	Asp	Pro
				260					265					270
Asp	Glu	Gly	Thr	Asn	Ala	Gln	Ile	Met	Tyr	Gln	Ile	Val	Glu	Gly
				275					280					285
Asn	Ile	Pro	Glu	Val	Phe	Gln	Leu	Asp	Ile	Phe	Ser	Gly	Glu	Leu
				290					295					300

Thr	Ala	Leu	Val	Asp	Leu	Asp	Tyr	Glu	Asp	Arg	Pro	Glu	Tyr	Val	305	310	315
Leu	Val	Ile	Gln	Ala	Thr	Ser	Ala	Pro	Leu	Val	Ser	Arg	Ala	Thr	320	325	330
Val	His	Val	Arg	Leu	Leu	Asp	Arg	Asn	Asp	Asn	Pro	Pro	Val	Leu	335	340	345
Gly	Asn	Phe	Glu	Ile	Leu	Phe	Asn	Asn	Tyr	Val	Thr	Asn	Arg	Ser	350	355	360
Ser	Ser	Phe	Pro	Gly	Gly	Ala	Ile	Gly	Arg	Val	Pro	Ala	His	Asp	365	370	375
Pro	Asp	Ile	Ser	Asp	Ser	Leu	Thr	Tyr	Ser	Phe	Glu	Arg	Gly	Asn	380	385	390
Glu	Leu	Ser	Leu	Val	Leu	Leu	Asn	Ala	Ser	Thr	Gly	Glu	Leu	Lys	395	400	405
Leu	Ser	Arg	Ala	Leu	Asp	Asn	Asn	Arg	Pro	Leu	Glu	Ala	Ile	Met	410	415	420
Ser	Val	Leu	Val	Ser	Asp	Gly	Val	His	Ser	Val	Thr	Ala	Gln	Cys	425	430	435
Ala	Leu	Arg	Val	Thr	Ile	Ile	Thr	Asp	Glu	Met	Leu	Thr	His	Ser	440	445	450
Ile	Thr	Leu	Arg	Leu	Glu	Asp	Met	Ser	Pro	Glu	Arg	Phe	Leu	Ser	455	460	465
Pro	Leu	Leu	Gly	Leu	Phe	Ile	Gln	Ala	Val	Ala	Ala	Thr	Leu	Ala	470	475	480
Thr	Pro	Pro	Asp	His	Val	Val	Val	Phe	Asn	Val	Gln	Arg	Asp	Thr	485	490	495
Asp	Ala	Pro	Gly	Gly	His	Ile	Leu	Asn	Val	Ser	Leu	Ser	Val	Gly	500	505	510
Gln	Pro	Pro	Gly	Pro	Gly	Gly	Gly	Pro	Pro	Phe	Leu	Pro	Ser	Glu	515	520	525
Asp	Leu	Gln	Glu	Arg	Leu	Tyr	Leu	Asn	Arg	Ser	Leu	Leu	Thr	Ala	530	535	540
Ile	Ser	Ala	Gln	Arg	Val	Leu	Pro	Phe	Asp	Asp	Asn	Ile	Cys	Leu	545	550	555
Arg	Glu	Pro	Cys	Glu	Asn	Tyr	Met	Arg	Cys	Val	Ser	Val	Leu	Arg	560	565	570
Phe	Asp	Ser	Ser	Ala	Pro	Phe	Ile	Ala	Ser	Ser	Ser	Val	Leu	Phe	575	580	585
Arg	Pro	Ile	His	Pro	Val	Gly	Gly	Leu	Arg	Cys	Arg	Cys	Pro	Pro	590	595	600
Gly	Phe	Thr	Gly	Asp	Tyr	Cys	Glu	Thr	Glu	Val	Asp	Leu	Cys	Tyr	605	610	615
Ser	Arg	Pro	Cys	Gly	Pro	His	Gly	Arg	Cys	Arg	Ser	Arg	Glu	Gly	620	625	630
Gly	Tyr	Thr	Cys	Leu	Cys	Arg	Asp	Gly	Tyr	Thr	Gly	Glu	His	Cys	635	640	645
Glu	Val	Ser	Ala	Arg	Ser	Gly	Arg	Cys	Thr	Pro	Gly	Val	Cys	Lys	650	655	660
Asn	Gly	Gly	Thr	Cys	Val	Asn	Leu	Leu	Val	Gly	Gly	Phe	Lys	Cys	665	670	675
Asp	Cys	Pro	Ser	Gly	Asp	Phe	Glu	Lys	Pro	Tyr	Cys	Gln	Val	Thr	680	685	690
Thr	Arg	Ser	Phe	Pro	Ala	His	Ser	Phe	Ile	Thr	Phe	Arg	Gly	Leu	695	700	705
Arg	Gln	Arg	Phe	His	Phe	Thr	Leu	Ala	Leu	Ser	Phe	Ala	Thr	Lys	710	715	720
Glu	Arg	Asp	Gly	Leu	Leu	Leu	Tyr	Asn	Gly	Arg	Phe	Asn	Glu	Lys	725	730	735
His	Asp	Phe	Val	Ala	Leu	Glu	Val	Ile	Gln	Glu	Gln	Val	Gln	Leu	740	745	750
Thr	Phe	Ser	Ala	Gly	Glu	Ser	Thr	Thr	Thr	Val	Ser	Pro	Phe	Val	755	760	765
Pro	Gly	Gly	Val	Ser	Asp	Gly	Gln	Trp	His	Thr	Val	Gln	Leu	Lys			

	770		775		780
Tyr Tyr Asn Lys	Pro Leu Leu Gly Gln Thr Gly Leu Pro Gln Gly				
	785		790		795
Pro Ser Glu Gln	Lys Val Ala Val Val Thr Val Asp Gly Cys Asp				
	800		805		810
Thr Gly Val Ala	Leu Arg Phe Gly Ser Val Leu Gly Asn Tyr Ser				
	815		820		825
Cys Ala Ala Gln	Gly Thr Gln Gly Gly Ser Lys Lys Ser Leu Asp				
	830		835		840
Leu Thr Gly Pro	Leu Leu Leu Gly Gly Val Pro Asp Leu Pro Glu				
	845		850		855
Ser Phe Pro Val	Arg Met Arg Gln Phe Val Gly Cys Met Arg Asn				
	860		865		870
Leu Gln Val Asp	Ser Arg His Ile Asp Met Ala Asp Phe Ile Ala				
	875		880		885
Asn Asn Gly Thr	Val Pro Gly Cys Pro Ala Lys Lys Asn Val Cys				
	890		895		900
Asp Ser Asn Thr	Cys His Asn Gly Gly Thr Cys Val Asn Gln Trp				
	905		910		915
Asp Ala Phe Ser	Cys Glu Cys Pro Leu Gly Phe Gly Gly Lys Ser				
	920		925		930
Cys Ala Gln Glu	Met Ala Asn Pro Gln His Phe Leu Gly Ser Ser				
	935		940		945
Leu Val Ala Trp	His Gly Leu Ser Leu Pro Ile Ser Gln Pro Trp				
	950		955		960
Tyr Leu Ser Leu	Met Phe Arg Thr Arg Gln Ala Asp Gly Val Leu				
	965		970		975
Leu Gln Ala Ile	Thr Arg Gly Arg Ser Thr Ile Thr Leu Gln Leu				
	980		985		990
Arg Glu Gly His	Val Met Leu Ser Val Glu Gly Thr Gly Leu Gln				
	995		1000		1005
Ala Ser Ser Leu	Arg Leu Glu Pro Gly Arg Ala Asn Asp Gly Asp				
	1010		1015		1020
Trp His His Ala	Gln Leu Ala Leu Gly Ala Ser Gly Gly Pro Gly				
	1025		1030		1035
His Ala Ile Leu	Ser Phe Asp Tyr Gly Gln Gln Arg Ala Glu Gly				
	1040		1045		1050
Asn Leu Gly Pro	Arg Leu His Gly Leu His Leu Ser Asn Ile Thr				
	1055		1060		1065
Val Gly Gly Ile	Pro Gly Pro Ala Gly Gly Val Ala Arg Gly Phe				
	1070		1075		1080
Arg Gly Cys Leu	Gln Gly Val Arg Val Ser Asp Thr Pro Glu Gly				
	1085		1090		1095
Val Asn Ser Leu	Asp Pro Ser His Gly Glu Ser Ile Asn Val Glu				
	1100		1105		1110
Gln Gly Cys Ser	Leu Pro Asp Pro Cys Asp Ser Asn Pro Cys Pro				
	1115		1120		1125
Ala Asn Ser Tyr	Cys Ser Asn Asp Trp Asp Ser Tyr Ser Cys Ser				
	1130		1135		1140
Cys Asp Pro Gly	Tyr Tyr Gly Asp Asn Cys Thr Asn Val Cys Asp				
	1145		1150		1155
Leu Asn Pro Cys	Glu His Gln Ser Val Cys Thr Arg Lys Pro Ser				
	1160		1165		1170
Ala Pro His Gly	Tyr Thr Cys Glu Cys Pro Pro Asn Tyr Leu Gly				
	1175		1180		1185
Pro Tyr Cys Glu	Thr Arg Ile Asp Gln Pro Cys Pro Arg Gly Trp				
	1190		1195		1200
Trp Gly His Pro	Thr Cys Gly Pro Cys Asn Cys Asp Val Ser Lys				
	1205		1210		1215
Gly Phe Asp Pro	Asp Cys Asn Lys Thr Ser Gly Glu Cys His Cys				
	1220		1225		1230
Lys Glu Asn His	Tyr Arg Pro Pro Gly Ser Pro Thr Cys Leu Leu				
	1235		1240		1245

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Cys Asp Cys Tyr Pro Thr Gly Ser Leu Ser Arg Val Cys Asp Pro 1250 1260  
 Glu Asp Gly Gln Cys Pro Cys Lys Pro Gly Val Ile Gly Arg Gln 1265 1270 1275  
 Cys Asp Arg Cys Asp Asn Pro Phe Ala Glu Val Thr Thr Asn Gly 1280 1285 1290  
 Cys Glu Val Asn Tyr Asp Ser Cys Pro Arg Ala Ile Glu Ala Gly 1295 1300 1305  
 Ile Trp Trp Pro Arg Thr Arg Phe Gly Leu Pro Ala Ala Ala Pro 1310 1315 1320  
 Cys Pro Lys Gly Ser Phe Gly Thr Ala Val Arg His Cys Asp Glu 1325 1330 1335  
 His Arg Gly Trp Leu Pro Pro Asn Leu Phe Asn Cys Thr Ser Ile 1340 1345 1350  
 Thr Phe Ser Glu Leu Lys Gly Phe Ala Glu Arg Leu Gln Arg Asn 1355 1360 1365  
 Glu Ser Gly Leu Asp Ser Gly Arg Ser Gln Gln Leu Ala Leu Leu 1370 1375 1380  
 Leu Arg Asn Ala Thr Gln His Thr Ala Gly Tyr Phe Gly Ser Asp 1385 1390 1395  
 Val Lys Val Ala Tyr Gln Leu Ala Thr Arg Leu Leu Ala His Glu 1400 1405 1410  
 Ser Thr Gln Arg Gly Phe Gly Leu Ser Ala Thr Gln Asp Val His 1415 1420 1425  
 Phe Thr Glu Asn Leu Leu Arg Val Gly Ser Ala Leu Leu Asp Thr 1430 1435 1440  
 Ala Asn Lys Arg His Trp Glu Leu Ile Gln Gln Thr Glu Gly Gly 1445 1450 1455  
 Thr Ala Trp Leu Leu Gln His Tyr Glu Ala Tyr Ala Ser Ala Leu 1460 1465 1470  
 Ala Gln Asn Met Arg His Thr Tyr Leu Ser Pro Phe Thr Ile Val 1475 1480 1485  
 Thr Pro Asn Ile Val Ile Ser Val Val Arg Leu Asp Lys Gly Asn 1490 1495 1500  
 Phe Ala Gly Ala Lys Leu Pro Arg Tyr Glu Ala Leu Arg Gly Glu 1505 1510 1515  
 Gln Pro Pro Asp Leu Glu Thr Thr Val Ile Leu Pro Glu Ser Val 1520 1525 1530  
 Phe Arg Glu Thr Pro Pro Val Val Arg Pro Ala Gly Pro Gly Glu 1535 1540 1545  
 Ala Gln Glu Pro Glu Glu Leu Ala Arg Arg Gln Arg Arg His Pro 1550 1555 1560  
 Glu Leu Ser Gln Gly Glu Ala Val Ala Ser Val Ile Ile Tyr Arg 1565 1570 1575  
 Thr Leu Ala Gly Leu Leu Pro His Asn Tyr Asp Pro Asp Lys Arg 1580 1585 1590  
 Ser Leu Arg Val Pro Lys Arg Pro Ile Ile Asn Thr Pro Val Val 1595 1600 1605  
 Ser Ile Ser Val His Asp Asp Glu Glu Leu Leu Pro Arg Ala Leu 1610 1615 1620  
 Asp Lys Pro Val Thr Val Gln Phe Arg Leu Leu Glu Thr Glu Glu 1625 1630 1635  
 Arg Thr Lys Pro Ile Cys Val Phe Trp Asn His Ser Ile Leu Val 1640 1645 1650  
 Ser Gly Thr Gly Gly Trp Ser Ala Arg Gly Cys Glu Val Val Phe 1655 1660 1665  
 Arg Asn Glu Ser His Val Ser Cys Gln Cys Asn His Met Thr Ser 1670 1675 1680  
 Phe Ala Val Leu Met Asp Val Ser Arg Arg Glu Asn Gly Glu Ile 1685 1690 1695  
 Leu Pro Leu Lys Thr Leu Thr Tyr Val Ala Leu Gly Val Thr Leu 1700 1705 1710  
 Ala Ala Leu Leu Leu Thr Phe Phe Phe Leu Thr Leu Leu Arg Ile

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	1715		1720		1725
Leu Arg Ser Asn Gln His Gly Ile Arg Arg Asn Leu Thr Ala Ala					
	1730		1735		1740
Leu Gly Leu Ala Gln Leu Val Phe Leu Leu Gly Ile Asn Gln Ala					
	1745		1750		1755
Asp Leu Pro Phe Ala Cys Thr Val Ile Ala Ile Leu Leu His Phe					
	1760		1765		1770
Leu Tyr Leu Cys Thr Phe Ser Trp Ala Leu Leu Glu Ala Leu His					
	1775		1780		1785
Leu Tyr Arg Ala Leu Thr Glu Val Arg Asp Val Asn Thr Gly Pro					
	1790		1795		1800
Met Arg Phe Tyr Tyr Met Leu Gly Trp Gly Val Pro Ala Phe Ile					
	1805		1810		1815
Thr Gly Leu Ala Val Gly Leu Asp Pro Glu Gly Tyr Gly Asn Pro					
	1820		1825		1830
Asp Phe Cys Trp Leu Ser Ile Tyr Asp Thr Leu Ile Trp Ser Phe					
	1835		1840		1845
Ala Gly Pro Val Ala Phe Ala Val Ser Met Ser Val Phe Leu Tyr					
	1850		1855		1860
Ile Leu Ala Ala Arg Ala Ser Cys Ala Ala Gln Arg Gln Gly Phe					
	1865		1870		1875
Glu Lys Lys Gly Pro Val Ser Gly Leu Gln Pro Ser Phe Ala Val					
	1880		1885		1890
Leu Leu Leu Leu Ser Ala Thr Trp Leu Leu Ala Leu Leu Ser Val					
	1895		1900		1905
Asn Ser Asp Thr Leu Leu Phe His Tyr Leu Phe Ala Thr Cys Asn					
	1910		1915		1920
Cys Ile Gln Gly Pro Phe Ile Phe Leu Ser Tyr Val Val Leu Ser					
	1925		1930		1935
Lys Glu Val Arg Lys Ala Leu Lys Leu Ala Cys Ser Arg Lys Pro					
	1940		1945		1950
Ser Pro Asp Pro Ala Leu Thr Thr Lys Ser Thr Leu Thr Ser Ser					
	1955		1960		1965
Tyr Asn Cys Pro Ser Pro Tyr Ala Asp Gly Arg Leu Tyr Gln Pro					
	1970		1975		1980
Tyr Gly Asp Ser Ala Gly Ser Leu His Ser Thr Ser Arg Ser Gly					
	1985		1990		1995
Lys Ser Gln Pro Ser Tyr Ile Pro Phe Leu Leu Arg Glu Glu Ser					
	2000		2005		2010
Ala Leu Asn Pro Gly Gln Gly Pro Pro Gly Leu Gly Asp Pro Gly					
	2015		2020		2025
Ser Leu Phe Leu Glu Gly Gln Asp Gln Gln His Asp Pro Asp Thr					
	2030		2035		2040
Asp Ser Asp Ser Asp Leu Ser Leu Glu Asp Asp Gln Ser Gly Ser					
	2045		2050		2055
Tyr Ala Ser Thr His Ser Ser Asp Ser Glu Glu Glu Glu Glu					
	2060		2065		2070
Glu Glu Glu Glu Ala Ala Phe Pro Gly Glu Gln Gly Trp Asp Ser					
	2075		2080		2085
Leu Leu Gly Pro Gly Ala Glu Arg Leu Pro Leu His Ser Thr Pro					
	2090		2095		2100
Lys Asp Gly Gly Pro Gly Pro Gly Lys Ala Pro Trp Pro Gly Asp					
	2105		2110		2115
Phe Gly Thr Thr Ala Lys Glu Ser Ser Gly Asn Gly Ala Pro Glu					
	2120		2125		2130
Glu Arg Leu Arg Glu Asn Gly Asp Ala Leu Ser Arg Glu Gly Ser					
	2135		2140		2145
Leu Gly Pro Leu Pro Gly Ser Ser Ala Gln Pro His Lys Gly Ile					
	2150		2155		2160
Leu Lys Lys Lys Cys Leu Pro Thr Ile Ser Glu Lys Ser Ser Leu					
	2165		2170		2175
Leu Arg Leu Pro Leu Glu Gln Cys Thr Gly Ser Ser Arg Gly Ser					
	2180		2185		2190



Ser Ala Ser Glu Gly Ser Arg Gly Gly Pro Pro Pro Arg Pro Pro  
 2195 2200 2205  
 Pro Arg Gln Ser Leu Gln Glu Gln Leu Asn Gly Val Met Pro Ile  
 2210 2215 2220  
 Ala Met Ser Ile Lys Ala Gly Thr Val Asp Glu Asp Ser Ser Gly  
 2225 2230 2235  
 Ser Glu Phe Leu Phe Phe Asn Phe Leu His  
 2240 2245

&lt;210&gt; 139

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:148485.8.orf1:2002JAN18

&lt;400&gt; 139

Ile Gly Met Ser Gly Leu Leu Thr Asp Pro Glu Gln Arg Ala Gln  
 1 5 10 15  
 Glu Pro Arg Tyr Pro Gly Phe Val Leu Gly Leu Asp Val Gly Ser  
 20 25 30  
 Ser Val Ile Arg Cys His Val Tyr Asp Arg Ala Ala Arg Val Cys  
 35 40 45  
 Gly Ser Ser Val Gln Lys Val Glu Asn Leu Tyr Pro Gln Ile Gly  
 50 55 60  
 Trp Val Glu Ile Asp Pro Asp Val Leu Trp Ile Gln Phe Val Ala  
 65 70 75  
 Val Ile Lys Glu Ala Val Lys Ala Ala Gly Ile Gln Met Asn Gln  
 80 85 90  
 Ile Val Gly Leu Gly Ile Ser Thr Gln Arg Ala Thr Phe Ile Thr  
 95 100 105  
 Trp Asn Lys Lys Thr Gly Asn His Phe His Asn Phe Ile Ser Trp  
 110 115 120  
 Gln Asp Leu Arg Ala Val Glu Leu Val Lys Ser Trp Asn Asn Ser  
 125 130 135  
 Leu Leu Met Lys Ile Phe His Ser Ser Cys Arg Val Leu His Phe  
 140 145 150  
 Phe Thr Arg Ser Lys Arg Leu Phe Thr Ala Ser Leu Phe Thr Phe  
 155 160 165  
 Thr Thr Gln Gln Thr Ser Leu Arg Leu Val Trp Ile Leu Gln Asn  
 170 175 180  
 Leu Thr Glu Val Gln Lys Ala Val Glu Glu Asn Cys Cys Phe  
 185 190 195  
 Gly Thr Ile Asp Thr Trp Leu Leu Tyr Lys Leu Thr Lys Gly Ser  
 200 205 210  
 Val Tyr Ala Thr Asp Phe Ser Asn Ala Ser Thr Thr Gly Leu Phe  
 215 220 225  
 Asp Pro Tyr Lys Met Cys Trp Ser Gly Met Ile Thr Ser Leu Ile  
 230 235 240  
 Ser Ile Pro Leu Ser Leu Leu Pro Pro Val Arg Asp Thr Ser His  
 245 250 255  
 Asn Phe Gly Ser Val Asp Glu Glu Ile Phe Gly Val Pro Ile Pro  
 260 265 270  
 Ile Val Ala Leu Val Ala Asp Gln Gln Ser Ala Met Phe Gly Glu  
 275 280 285  
 Cys Cys Phe Gln Thr Gly Asp Val Lys Leu Thr Met Gly Thr Gly  
 290 295 300  
 Thr Phe Leu Asp Ile Asn Thr Gly Asn Ser Leu Gln Gln Thr Thr  
 305 310 315  
 Gly Gly Phe Tyr Pro Leu Ile Gly Trp Lys Ile Gly Gln Glu Val  
 320 325 330

Val	Cys	Leu	Ala	Glu	Ser	Asn	Ala	Gly	Asp	Thr	Gly	Thr	Ala	Ile
				335					340					345
Lys	Trp	Ala	Gln	Gln	Leu	Asp	Leu	Phe	Thr	Asp	Ala	Ala	Glu	Thr
				350					355					360
Glu	Lys	Met	Ala	Lys	Ser	Leu	Glu	Asp	Ser	Glu	Gly	Val	Cys	Phe
				365					370					375
Val	Pro	Ser	Phe	Ser	Gly	Leu	Gln	Ala	Pro	Leu	Asn	Asp	Pro	Trp
				380					385					390
Ala	Cys	Ala	Ser	Phe	Met	Gly	Leu	Lys	Pro	Ser	Thr	Ser	Lys	Tyr
				395					400					405
His	Leu	Val	Arg	Ala	Ile	Leu	Glu	Ser	Ile	Ala	Phe	Arg	Asn	Lys
				410					415					420
Gln	Leu	Tyr	Glu	Met	Met	Lys	Lys	Glu	Ile	His	Ile	Pro	Val	Arg
				425					430					435
Lys	Ile	Arg	Ala	Asp	Gly	Gly	Val	Cys	Lys	Asn	Gly	Phe	Val	Met
				440					445					450
Gln	Met	Thr	Ser	Asp	Leu	Ile	Asn	Glu	Asn	Ile	Asp	Arg	Pro	Ala
				455					460					465
Asp	Ile	Asp	Met	Ser	Cys	Leu	Gly	Ala	Ala	Ser	Leu	Ala	Gly	Leu
				470					475					480
Ala	Val	Gly	Phe	Gly	Leu	Thr	Arg	Arg	Asn					
				485					490					

&lt;210&gt; 140

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1502670.1.orf2:2002JAN18

&lt;400&gt; 140

Ala	Leu	Ser	Arg	Gly	Ala	Glu	Leu	Arg	Val	Pro	Gly	Gly	Ala	Lys
1				5					10					15
His	Gly	Met	Cys	Leu	Leu	Leu	Gly	Ala	Thr	Gly	Val	Gly	Lys	Thr
				20					25					30
Leu	Leu	Val	Lys	Arg	Leu	Gln	Glu	Val	Ser	Ser	Arg	Asp	Gly	Lys
				35					40					45
Gly	Asp	Leu	Gly	Glu	Pro	Pro	Pro	Thr	Arg	Pro	Thr	Val	Gly	Thr
				50					55					60
Asn	Leu	Thr	Asp	Ile	Val	Ala	Gln	Arg	Lys	Ile	Thr	Ile	Arg	Glu
				65					70					75
Leu	Gly	Gly	Cys	Met	Gly	Pro	Ile	Trp	Ser	Ser	Tyr	Tyr	Gly	Asn
				80					85					90
Cys	Arg	Ser	Leu	Leu	Phe	Val	Met	Asp	Ala	Ser	Asp	Pro	Thr	Gln
				95					100					105
Leu	Ser	Ala	Ser	Cys	Val	Gln	Leu	Leu	Gly	Leu	Leu	Ser	Ala	Glu
				110					115					120
Gln	Leu	Ala	Glu	Ala	Ser	Val	Leu	Ile	Leu	Phe	Asn	Lys	Ile	Asp
				125					130					135
Leu	Pro	Cys	Tyr	Met	Ser	Thr	Glu	Glu	Met	Lys	Ser	Leu	Ile	Arg
				140					145					150
Leu	Pro	Asp	Ile	Ile	Ala	Cys	Ala	Lys	Gln	Asn	Ile	Thr	Thr	Ala
				155					160					165
Glu	Ile	Ser	Ala	Arg	Glu	Gly	Thr	Gly	Leu	Ala	Gly	Val	Leu	Ala
				170					175					180
Trp	Leu	Gln	Ala	Thr	His	Arg	Ala	Asn	Asp					
				185					190					

&lt;210&gt; 141

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:206593.3.orf2:2002JAN18

&lt;400&gt; 141

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Leu Ser Thr Tyr Glu Leu Thr Leu Glu Arg Lys Pro Tyr Glu Cys
 1          5          10          15
Lys Val Cys Gly Lys Ala Phe Thr Thr Ser Ser His Leu Ile Val
          20          25          30
His Ile Arg Ser His Thr Gly Glu Lys Pro Tyr Ile Cys Lys Glu
          35          40          45
Cys Gly Lys Ala Phe Ala Ser Ser Ser His Leu Ile Glu His Arg
          50          55          60
Arg Thr His Thr Gly Glu Lys Pro Tyr Ile Cys Asn Glu Cys Gly
          65          70          75
Lys Ala Phe Arg Ala Ser Ser His Leu His Lys His Gly Arg Ile
          80          85          90
His Thr Gly Gln Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala
          95          100         105
Tyr Asn Arg Phe Tyr Leu Leu Lys Glu His Leu Lys Thr Tyr Thr
          110         115         120
Glu Glu Gln Val Phe Val Cys Lys Asp Cys Gly Lys Ser Phe Lys
          125         130         135
Asn Ser Ser Cys Leu Asn His His Thr Gln Ile His Thr Asp Glu
          140         145         150
Lys Pro Phe

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&lt;210&gt; 142

&lt;211&gt; 608

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:228273.22.orf1:2002JAN18

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1) ... (608)

&lt;223&gt; unknown or other

&lt;400&gt; 142

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Gly Pro Gly Ser Asp Pro Arg Ala Ser Ser Gln Thr Met Arg Arg
 1          5          10          15
Arg Ser Trp Asp Gln Ala Cys Leu Leu Gln Glu Lys Gln Glu Glu
          20          25          30
Gly Lys Asp Pro Glu Gly Gln Pro Leu Leu Ala Pro Gln Arg Val
          35          40          45
Arg Ser Gly Ala Ala Ala Xaa Leu Gln Gln Val Arg Thr Lys Glu
          50          55          60
Cys Trp Ser Trp Glu Ser Tyr Leu Glu Glu Gln Lys Ala Ile Thr
          65          70          75
Ala Pro Val Ser Leu Phe Gln Asp Ser Gln Ala Val Thr His Asn
          80          85          90
Lys Asn Gly Phe Lys Leu Gly Met Lys Leu Glu Gly Ile Asp Pro
          95          100         105
Gln His Pro Ser Met Tyr Phe Ile Leu Thr Val Ala Glu Val Cys
          110         115         120
Gly Tyr Arg Leu Arg Leu His Phe Asp Gly Tyr Ser Glu Cys His
          125         130         135

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Asp	Phe	Trp	Val	Asn	Ala	Asn	Ser	Pro	Asp	Ile	His	Pro	Ala	Gly
				140					145					150
Trp	Phe	Glu	Lys	Thr	Gly	His	Lys	Leu	Gln	Pro	Pro	Lys	Gly	Tyr
				155					160					165
Lys	Glu	Glu	Glu	Phe	Ser	Trp	Ser	Gln	Tyr	Leu	Arg	Ser	Thr	Arg
				170					175					180
Ala	Gln	Ala	Ala	Pro	Lys	His	Leu	Phe	Val	Ser	Gln	Ser	His	Ser
				185					190					195
Pro	Pro	Pro	Leu	Gly	Phe	Gln	Val	Gly	Met	Lys	Leu	Glu	Ala	Val
				200					205					210
Asp	Arg	Met	Asn	Pro	Ser	Leu	Val	Cys	Val	Ala	Ser	Val	Thr	Asp
				215					220					225
Val	Val	Asp	Ser	Arg	Phe	Leu	Val	His	Phe	Asp	Asn	Trp	Asp	Asp
				230					235					240
Thr	Tyr	Asp	Tyr	Trp	Cys	Asp	Pro	Ser	Ser	Pro	Tyr	Ile	His	Pro
				245					250					255
Val	Gly	Trp	Cys	Gln	Lys	Gln	Gly	Lys	Pro	Leu	Thr	Pro	Pro	Gln
				260					265					270
Asp	Tyr	Pro	Asp	Pro	Asp	Asn	Phe	Cys	Trp	Glu	Lys	Tyr	Leu	Glu
				275					280					285
Glu	Thr	Gly	Ala	Ser	Ala	Val	Pro	Thr	Trp	Ala	Phe	Lys	Val	Arg
				290					295					300
Pro	Pro	His	Ser	Phe	Leu	Val	Asn	Met	Lys	Leu	Glu	Ala	Val	Asp
				305					310					315
Arg	Arg	Asn	Pro	Ala	Leu	Ile	Arg	Val	Ala	Ser	Val	Glu	Asp	Val
				320					325					330
Glu	Asp	His	Arg	Ile	Lys	Ile	His	Phe	Asp	Gly	Trp	Ser	His	Gly
				335					340					345
Tyr	Asp	Phe	Trp	Ile	Asp	Ala	Asp	His	Pro	Asp	Ile	His	Pro	Ala
				350					355					360
Gly	Trp	Cys	Ser	Lys	Thr	Gly	His	Pro	Leu	Gln	Pro	Pro	Leu	Gly
				365					370					375
Pro	Arg	Glu	Pro	Ser	Ser	Ala	Ser	Pro	Gly	Gly	Cys	Pro	Pro	Leu
				380					385					390
Ser	Tyr	Arg	Ser	Leu	Pro	His	Thr	Arg	Thr	Ser	Lys	Tyr	Ser	Phe
				395					400					405
His	His	Arg	Lys	Cys	Pro	Thr	Pro	Gly	Cys	Asp	Gly	Ser	Gly	His
				410					415					420
Val	Thr	Gly	Lys	Phe	Thr	Ala	His	His	Cys	Leu	Ser	Gly	Cys	Pro
				425					430					435
Leu	Ala	Glu	Arg	Asn	Gln	Ser	Arg	Leu	Lys	Ala	Glu	Leu	Ser	Asp
				440					445					450
Ser	Glu	Ala	Ser	Ala	Arg	Lys	Lys	Asn	Leu	Ser	Gly	Phe	Ser	Pro
				455					460					465
Arg	Lys	Lys	Pro	Arg	His	His	Gly	Arg	Ile	Gly	Arg	Pro	Pro	Lys
				470					475					480
Tyr	Arg	Lys	Ile	Pro	Gln	Glu	Asp	Phe	Gln	Thr	Leu	Thr	Pro	Asp
				485					490					495
Val	Val	His	Gln	Ser	Leu	Phe	Met	Ser	Ala	Leu	Ser	Ala	His	Pro
				500					505					510
Asp	Arg	Ser	Leu	Ser	Val	Cys	Trp	Glu	Gln	His	Cys	Lys	Leu	Leu
				515					520					525
Pro	Gly	Val	Ala	Gly	Ile	Ser	Ala	Ser	Thr	Val	Ala	Lys	Trp	Thr
				530					535					540
Ile	Asp	Glu	Val	Phe	Gly	Phe	Val	Gln	Thr	Leu	Thr	Gly	Cys	Glu
				545					550					555
Asp	Gln	Ala	Arg	Leu	Phe	Lys	Asp	Glu	Met	Ile	Asp	Gly	Glu	Ala
				560					565					570
Phe	Leu	Leu	Leu	Thr	Gln	Ala	Asp	Ile	Val	Lys	Ile	Met	Ser	Val
				575					580					585
Lys	Leu	Gly	Pro	Ala	Leu	Lys	Ile	Tyr	Asn	Ala	Ile	Leu	Met	Phe
				590					595					600
Lys	Asn	Ala	Asp	Asp	Thr	Leu	Lys							

605

<210> 143  
 <211> 265  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:228319.2.orf1:2002JAN18

<400> 143  
 Glu Gln Ala Glu Glu Glu Lys Lys Pro Lys Asp Ser Thr Thr Pro  
 1 5 10 15  
 Leu Ser His Val Pro Ser Ala Ala Ala Gln Gly Ala Trp Ser Trp  
 20 25 30  
 Glu Trp Tyr Leu Lys Glu Gln Lys Ala Val Ala Ala Pro Val Glu  
 35 40 45  
 Leu Phe Ser Lys Asp Gln Ser Phe Pro Glu His Glu Asn Gly Phe  
 50 55 60  
 Gln Ile Gly Met Arg Leu Glu Gly Ile Asp Pro Arg His Pro Ser  
 65 70 75  
 Val Phe Cys Val Leu Ser Val Ala Glu Val Cys Gly Tyr Arg Leu  
 80 85 90  
 Arg Leu His Phe Asp Gly Tyr Leu Ser Cys Tyr Asp Phe Trp Thr  
 95 100 105  
 Asn Ala Gly Ser Pro Asp Ile His Pro Val Gly Trp Cys Glu Lys  
 110 115 120  
 Thr Lys His Glu Leu His Ile Pro Lys Gly Tyr Arg Lys Asp Lys  
 125 130 135  
 Phe Val Trp Met Asp Tyr Leu Lys Ala Cys Lys Leu Gln Asn Ala  
 140 145 150  
 Pro Lys Lys Leu Phe Arg Asn Arg Ser Pro Asn Gly Pro Met Ser  
 155 160 165  
 Lys Glu Phe Gln Val Gly Met Lys Leu Glu Ala Val Asp Arg Lys  
 170 175 180  
 Asn Pro Ser Leu Val Cys Val Ala Thr Ile Ala Asp Ile Val Glu  
 185 190 195  
 Asp Arg Leu Leu Val His Phe Asp Asn Trp Gly Asp Ser Tyr Asp  
 200 205 210  
 Tyr Trp Cys Asp Val Asn Ser Pro Tyr Val Gln Pro Val Gly Trp  
 215 220 225  
 Cys Gln Glu Asn Gly Arg Thr Leu Ile Ala Pro Gln Gly Tyr Pro  
 230 235 240  
 Ile Gln Lys Ile Phe Pro Gly Gln Asn Thr Trp Lys Leu Leu Lys  
 245 250 255  
 Pro Met Gln Phe Leu Pro Lys Phe Leu Lys  
 260 265

<210> 144  
 <211> 687  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:229165.16.orf2:2002JAN18

<400> 144  
 Tyr Gln Arg Gln Leu Lys Glu Met Asn Phe Glu Thr Ser Arg Cys  
 1 5 10 15  
 Ala Thr Leu Gln Tyr Cys Pro Asp Pro Tyr Ile Gln Arg Phe Val  
 20 25 30

142/218

Glu	Thr	Pro	Ala	His	Phe	Ser	Trp	Lys	Glu	Ser	Tyr	Tyr	Arg	Ser
				35					40					45
Thr	Met	Ser	Gln	Ser	Thr	Gln	Thr	Asn	Glu	Phe	Leu	Ser	Pro	Glu
				50					55					60
Val	Phe	Gln	His	Ile	Trp	Asp	Phe	Leu	Glu	Gln	Pro	Ile	Cys	Ser
				65					70					75
Val	Gln	Pro	Ile	Asp	Leu	Asn	Phe	Val	Asp	Glu	Pro	Ser	Glu	Asp
				80					85					90
Gly	Ala	Thr	Asn	Lys	Ile	Glu	Ile	Ser	Met	Asp	Cys	Ile	Arg	Met
				95					100					105
Gln	Asp	Ser	Asp	Leu	Ser	Asp	Pro	Met	Trp	Pro	Gln	Tyr	Thr	Asn
				110					115					120
Leu	Gly	Leu	Leu	Asn	Ser	Met	Asp	Gln	Gln	Ile	Gln	Asn	Gly	Ser
				125					130					135
Ser	Ser	Thr	Ser	Pro	Tyr	Asn	Thr	Asp	His	Ala	Gln	Asn	Ser	Val
				140					145					150
Thr	Ala	Pro	Ser	Pro	Tyr	Ala	Gln	Pro	Ser	Ser	Thr	Phe	Asp	Ala
				155					160					165
Leu	Ser	Pro	Ser	Pro	Ala	Ile	Pro	Ser	Asn	Thr	Asp	Tyr	Pro	Gly
				170					175					180
Pro	His	Ser	Phe	Asp	Val	Ser	Phe	Gln	Gln	Ser	Ser	Thr	Ala	Lys
				185					190					195
Ser	Ala	Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys	Lys	Leu	Tyr	Cys
				200					205					210
Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val	Met	Thr	Pro
				215					220					225
Pro	Pro	Gln	Gly	Ala	Val	Ile	Arg	Ala	Met	Pro	Val	Tyr	Lys	Lys
				230					235					240
Ala	Glu	His	Val	Thr	Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His	Glu
				245					250					255
Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His
				260					265					270
Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His	Ala	Gln	Tyr	Val	Glu	Asp
				275					280					285
Pro	Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val	Pro	Tyr	Glu	Pro	Pro
				290					295					300
Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Val	Leu	Tyr	Asn	Phe	Met	Cys
				305					310					315
Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Ile
				320					325					330
Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg
				335					340					345
Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys
				350					355					360
Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp	Ser	Thr
				365					370					375
Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr	His
				380					385					390
Gly	Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp
				395					400					405
Glu	Leu	Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met
				410					415					420
Leu	Leu	Lys	Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro
				425					430					435
Gln	His	Thr	Ile	Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His
				440					445					450
Gln	His	Leu	Leu	Gln	Lys	Gln	Thr	Ser	Ile	Gln	Ser	Pro	Ser	Ser
				455					460					465
Tyr	Gly	Asn	Ser	Ser	Pro	Pro	Leu	Asn	Lys	Met	Asn	Ser	Met	Asn
				470					475					480
Lys	Leu	Pro	Ser	Val	Ser	Gln	Leu	Ile	Asn	Pro	Gln	Gln	Arg	Asn
				485					490					495
Ala	Leu	Thr	Pro	Thr	Thr	Ile	Pro	Asp	Gly	Met	Gly	Ala	Asn	Ile

Pro Met Met Gly	500	Thr His Met Pro Met	505	Ala Gly Asp Met Asn Gly	510
	515		520		525
Leu Ser Pro Thr	530	Gln Ala Leu Pro Pro	535	Pro Leu Ser Met Pro Ser	540
Thr Ser His Cys	545	Thr Pro Pro Pro Pro	550	Tyr Pro Thr Asp Cys Ser	555
Ile Val Ser Phe	560	Leu Ala Arg Leu Gly	565	Cys Ser Ser Cys Leu Asp	570
Tyr Phe Thr Thr	575	Gln Gly Leu Thr Thr	580	Ile Tyr Gln Ile Glu His	585
Tyr Ser Met Asp	590	Asp Leu Ala Ser Leu	595	Lys Ile Pro Glu Gln Phe	600
Arg His Ala Ile	605	Trp Lys Gly Ile Leu	610	Asp His Arg Gln Leu His	615
Glu Phe Ser Ser	620	Pro Ser His Leu Leu	625	Arg Thr Pro Ser Ser Ala	630
Ser Thr Val Ser	635	Val Gly Ser Ser Glu	640	Thr Arg Gly Glu Arg Val	645
Ile Asp Ala Val	650	Arg Phe Thr Leu Arg	655	Gln Thr Ile Ser Phe Pro	660
Pro Arg Asp Glu	665	Trp Asn Asp Phe Asn	670	Phe Asp Met Asp Ala Arg	675
Arg Asn Lys Gln	680	Gln Arg Ile Lys Glu	685	Glu Gly Glu	

&lt;210&gt; 145

&lt;211&gt; 478

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:230895.9.orf1:2002JAN18

&lt;400&gt; 145

Asn Arg Ser Leu Pro	Asp Val Arg Leu Glu	Gly Cys Lys Thr Lys
1	5	10
Val Tyr Pro Asp Glu	Leu Pro Asn Thr Ser	Val Val Ile Val Phe
	20	25
His Asn Glu Ala Trp	Ser Thr Leu Leu Arg	Thr Val Tyr Ser Val
	35	40
Ile Asn Arg Ser Pro	His Tyr Leu Leu Ser	Glu Val Ile Leu Val
	50	55
Asp Asp Ala Ser Glu	Arg Asp Phe Leu Lys	Leu Thr Leu Glu Asn
	65	70
Tyr Val Lys Asn Leu	Glu Val Pro Val Lys	Ile Ile Arg Met Glu
	80	85
Glu Arg Ser Gly Leu	Ile Arg Ala Arg Leu	Arg Gly Ala Ala Ala
	95	100
Ser Lys Gly Gln Val	Ile Thr Phe Leu Asp	Ala His Cys Glu Cys
	110	115
Thr Leu Gly Trp Leu	Glu Pro Leu Leu Ala	Arg Ile Lys Glu Asp
	125	130
Arg Lys Thr Val Val	Cys Pro Ile Ile Asp	Val Ile Ser Asp Asp
	140	145
Thr Phe Glu Tyr Met	Ala Gly Ser Asp Met	Thr Tyr Gly Gly Phe
	155	160
Asn Trp Lys Leu Asn	Phe Arg Trp Tyr Pro	Val Pro Gln Arg Glu
	170	175
Met Asp Arg Arg Lys	Gly Asp Arg Thr Leu	Pro Val Arg Thr Pro
	185	190
Thr Met Ala Gly Gly	Leu Phe Ser Ile Asp	Arg Asn Tyr Phe Glu

Glu Ile Gly Thr	200	Tyr Asp Ala Gly Met	205	Asp Ile Trp Gly Gly	210
	215		220		225
Asn Leu Glu Met	230	Ser Phe Arg Ile Trp	235	Gln Cys Gly Gly Ser	240
Glu Ile Val Thr	245	Cys Ser His Val Gly	250	His Val Phe Arg Lys	255
Thr Pro Tyr Thr	260	Phe Pro Gly Gly Thr	265	Gly His Val Ile Asn	270
Asn Asn Arg Arg	275	Leu Ala Glu Val Trp	280	Met Asp Glu Phe Lys	285
Phe Phe Tyr Ile	290	Ile Ser Pro Gly Val	295	Val Lys Val Asp Tyr	300
Asp Val Ser Val	305	Arg Lys Thr Leu Arg	310	Glu Asn Leu Lys Cys	315
Pro Phe Ser Trp	320	Tyr Leu Glu Asn Ile	325	Tyr Pro Asp Ser Gln	330
Pro Arg Arg Tyr	335	Tyr Ser Leu Gly Glu	340	Ile Arg Asn Val Glu	345
Asn Gln Cys Leu	350	Asp Asn Met Gly Arg	355	Lys Glu Asn Glu Lys	360
Gly Ile Phe Asn	365	Cys His Gly Met Gly	370	Gly Asn Gln Val Phe	375
Tyr Thr Ala Asp	380	Lys Glu Ile Arg Thr	385	Asp Asp Leu Cys Leu	390
Val Ser Arg Leu	395	Asn Gly Pro Val Ile	400	Met Leu Lys Cys His	405
Met Arg Gly Asn	410	Gln Leu Trp Glu Tyr	415	Asp Ala Glu Thr His	420
Leu Leu His Ile	425	Ile Thr Gln Ser Cys	430	Leu Ser Val Asn Lys	435
Ala Asp Gly Ser	440	Gln His Pro Thr Val	445	Glu Thr Cys Asn Asp	450
Thr Leu Gln Lys	455	Trp Leu Leu Arg Asn	460	Tyr Thr Arg Met Glu	465
Phe Arg Asn Ile	470	Phe Gly Asn Ser Thr	475	Asp Tyr Ile Leu	

&lt;210&gt; 146

&lt;211&gt; 946

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:233552.5.orf1:2002JAN18

&lt;400&gt; 146

Val Met Phe Ala Asp	Arg Lys Ser Lys	Leu Ser Arg Glu Phe Arg
1	5	10
Ala Leu Gly Thr Cys	Tyr Leu Asp Gln	Phe Glu Ala Ser Leu Ile
20	25	30
Tyr Trp Thr Asn Trp	Gln Gln Lys Met	Lys Ser Ser Val Ala Gln
35	40	45
Ile Lys Pro Ser Ser	Gly His Asp Arg	Arg Glu Asn Leu Asn Pro
50	55	60
Tyr Gln Arg Asn Ser	Ser Pro Glu Asp	Arg Tyr Glu Glu Gln Glu
65	70	75
Arg Ser Pro Arg Asp	Arg Asp Tyr Phe	Asp Tyr Ser Arg Ser Asp
80	85	90
Tyr Glu His Ser Arg	Arg Gly Arg Ser	Tyr Asp Ser Ser Met Glu
95	100	105
Ser Arg Asn Arg Asp	Arg Glu Lys Arg	Arg Glu Arg Glu Arg Asp



Thr Asp Arg Lys	110	Arg Ser Arg Lys Ser	115	Ser Pro Gly Arg	120
Asn Pro Glu Thr	125	Ser Val Thr Gln Ser	130	Ser Ser Ala Gln Asp	135
Pro Ala Thr Lys	140	Lys Lys Lys Asp Glu	145	Leu Asp Pro Leu Leu	150
Arg Thr Gly Gly	155	Ala Tyr Ile Pro Pro	160	Lys Leu Arg Met	165
Gln Glu Gln Ile	170	Thr Asp Lys Asn Ser	175	Leu Ala Tyr Gln Arg	180
Ser Trp Glu Ala	185	Leu Lys Lys Ser Ile	190	Asn Gly Leu Ile Asn	195
Val Asn Ile Ser	200	Asn Ile Ser Ile Ile	205	Gln Glu Leu Leu	210
Glu Asn Ile Val	215	Arg Gly Arg Gly Leu	220	Ser Arg Ser Val	225
Gln Ala Gln Ser	230	Ala Ser Pro Ile Phe	235	Thr His Val Tyr Ala	240
Leu Val Ala Ile	245	Ile Asn Ser Lys Phe	250	Pro Gln Ile Gly Glu	255
Ile Leu Lys Arg	260	Leu Ile Leu Asn Phe	265	Arg Lys Gly Tyr Arg	270
Asn Asp Lys Gln	275	Leu Cys Leu Thr Ala	280	Ser Lys Phe Val Ala	285
Leu Ile Asn Gln	290	Asn Val Ala His Glu	295	Val Leu Cys Leu Glu	300
Leu Thr Leu Leu	305	Leu Glu Arg Pro Thr	310	Asp Asp Ser Val Glu	315
Ala Ile Gly Phe	320	Leu Lys Glu Cys Gly	325	Leu Lys Leu Thr Gln	330
Ser Pro Arg Gly	335	Ile Asn Ala Ile Phe	340	Glu Arg Leu Arg Asn	345
Leu His Glu Ser	350	Glu Ile Asp Lys Arg	355	Val Gln Tyr Met Ile	360
Val Met Phe Ala	365	Val Arg Lys Asp Gly	370	Phe Lys Asp His Pro	375
Ile Leu Glu Gly	380	Leu Asp Leu Val Glu	385	Glu Asp Asp Gln Phe	390
His Met Leu Pro	395	Leu Glu Asp Asp Tyr	400	Asn Pro Glu Asp Val	405
Asn Val Phe Lys	410	Met Asp Pro Asn Phe	415	Met Glu Asn Glu Glu	420
Tyr Lys Ala Ile	425	Lys Lys Glu Ile Leu	430	Asp Glu Gly Asp Thr	435
Ser Asn Thr Asp	440	Gln Asp Ala Gly Ser	445	Ser Glu Glu Asp Glu	450
Glu Glu Glu Glu	455	Glu Gly Glu Glu Asp	460	Glu Glu Gly Gln Lys	465
Thr Ile His Asp	470	Lys Thr Glu Ile Asn	475	Leu Val Ser Phe Arg	480
Thr Ile Tyr Leu	485	Ala Ile Gln Ser Ser	490	Leu Asp Phe Glu Glu	495
Ala His Lys Leu	500	Leu Lys Met Glu Phe	505	Pro Glu Ser Gln Thr	510
Glu Leu Cys Asn	515	Met Ile Leu Asp Cys	520	Cys Ala Gln Gln Arg	525
Tyr Glu Lys Phe	530	Phe Gly Leu Leu Ala	535	Gly Arg Phe Cys Met	540
Lys Lys Glu Tyr	545	Met Glu Ser Phe Glu	550	Gly Ile Phe Lys Glu	555
Tyr Asp Thr Ile	560	His Arg Leu Glu Thr	565	Asn Lys Leu Arg Asn	570
	575		580		585

Ala	Lys	Met	Phe	Ala	His	Leu	Leu	Tyr	Thr	Asp	Ser	Leu	Pro	Trp	
				590					595					600	
Ser	Val	Leu	Glu	Cys	Ile	Lys	Leu	Ser	Glu	Glu	Thr	Thr	Thr	Ser	
				605					610					615	
Ser	Ser	Arg	Ile	Phe	Val	Lys	Ile	Phe	Phe	Gln	Glu	Leu	Cys	Glu	
				620					625					630	
Tyr	Met	Gly	Leu	Pro	Lys	Leu	Asn	Ala	Arg	Leu	Lys	Asp	Glu	Thr	
				635					640					645	
Leu	Gln	Pro	Phe	Phe	Glu	Gly	Leu	Leu	Pro	Arg	Asp	Asn	Pro	Arg	
				650					655					660	
Asn	Thr	Arg	Phe	Ala	Ile	Asn	Phe	Phe	Thr	Ser	Ile	Gly	Leu	Gly	
				665					670					675	
Gly	Leu	Thr	Asp	Glu	Leu	Arg	Glu	His	Leu	Lys	Asn	Thr	Pro	Lys	
				680					685					690	
Val	Ile	Val	Ala	Gln	Lys	Pro	Asp	Val	Glu	Gln	Asn	Lys	Ser	Ser	
				695					700					705	
Pro	Ser	Ser	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Glu	Ser	Asp	Ser	
				710					715					720	
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ser	Asp	Ser	Ser	Ser	Glu	Ser	Ser	
				725					730					735	
Ser	Glu	Glu	Ser	Asp	Ser	Ser	Ser	Ile	Ser	Ser	His	Ser	Ser	Ala	
				740					745					750	
Ser	Ala	Asn	Asp	Val	Arg	Lys	Lys	Gly	His	Gly	Lys	Thr	Arg	Ser	
				755					760					765	
Lys	Glu	Val	Asp	Lys	Leu	Ile	Arg	Asn	Gln	Gln	Thr	Asn	Asp	Arg	
				770					775					780	
Lys	Gln	Lys	Glu	Arg	Arg	Gln	Glu	His	Gly	His	Gln	Glu	Thr	Arg	
				785					790					795	
Thr	Glu	Arg	Glu	Arg	Arg	Ser	Glu	Lys	His	Arg	Asp	Gln	Asn	Ser	
				800					805					810	
Arg	Gly	Ser	Asn	Trp	Arg	Asp	Pro	Ile	Thr	Lys	Tyr	Thr	Ser	Asp	
				815					820					825	
Lys	Asp	Val	Pro	Ser	Glu	Arg	Asn	Asn	Tyr	Ser	Arg	Val	Ala	Asn	
				830					835					840	
Asp	Arg	Asp	Gln	Glu	Met	His	Ile	Asp	Leu	Glu	Asn	Lys	His	Gly	
				845					850					855	
Asp	Pro	Lys	Lys	Lys	Arg	Gly	Glu	Arg	Arg	Asn	Ser	Phe	Ser	Glu	
				860					865					870	
Asn	Glu	Lys	His	Thr	His	Arg	Ile	Lys	Asp	Ser	Glu	Asn	Phe	Arg	
				875					880					885	
Arg	Lys	Asp	Arg	Ser	Lys	Ser	Lys	Glu	Met	Asn	Arg	Lys	His	Ser	
				890					895					900	
Gly	Ser	Arg	Ser	Asp	Glu	Asp	Arg	Tyr	Gln	Asn	Gly	Ala	Glu	Arg	
				905					910					915	
Arg	Trp	Glu	Lys	Ser	Ser	Arg	Tyr	Ser	Glu	Gln	Ser	Arg	Glu	Ser	
				920					925					930	
Lys	Lys	Asn	Gln	Asp	Arg	Arg	Arg	Glu	Lys	Ser	Pro	Ala	Lys	Gln	
				935					940					945	
Lys															

&lt;210&gt; 147

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:234430.7.orf3:2002JAN18

&lt;400&gt; 147

Gly	Val	Glu	Ser	Ala	Pro	Cys	Pro	Arg	Arg	Glu	Arg	Gly	Ala	Gly	
1				5					10					15	

<400> 148															
Glu	Val	Arg	Ala	Ala	Gly	Ala	Glu	Ala	Thr	Ala	Ala	Ala	Ala	Ala	Ala
1				5					10						15
Gly	Gly	Ala	Ile	Ala	Ala	Ala	Val	Ala	Ala	Thr	Gly	Arg	Gly	Ala	
				20					25						30
Ala	Val	Gly	Asp	Arg	Gly	Arg	Gly	Cys	Arg	Arg	Arg	Ser	Gly	Trp	
				35					40						45
Lys	Lys	Leu	Asp	Ser	Met	Gly	Ser	Lys	Arg	Arg	Arg	Ala	Thr	Ser	
				50					55						60
Pro	Ser	Ser	Ser	Val	Ser	Gly	Asp	Phe	Asp	Asp	Gly	His	His	Ser	
				65					70						75

Val	Ser	Thr	Pro	Gly	Pro	Ser	Arg	Lys	Arg	Arg	Arg	Leu	Ser	Asn
				80					85					90
Leu	Pro	Thr	Val	Asp	Pro	Ile	Ala	Val	Cys	His	Glu	Leu	Tyr	Asn
				95					100					105
Thr	Ile	Arg	Asp	Tyr	Lys	Asp	Glu	Gln	Gly	Arg	Leu	Leu	Cys	Glu
				110					115					120
Leu	Phe	Ile	Arg	Ala	Pro	Lys	Arg	Arg	Asn	Gln	Pro	Asp	Tyr	Tyr
				125					130					135
Glu	Val	Val	Ser	Gln	Pro	Ile	Asp	Leu	Met	Lys	Ile	Gln	Gln	Lys
				140					145					150
Leu	Lys	Met	Glu	Glu	Tyr	Asp	Asp	Val	Asn	Leu	Leu	Thr	Ala	Asp
				155					160					165
Phe	Gln	Leu	Leu	Phe	Asn	Asn	Ala	Lys	Ser	Tyr	Tyr	Lys	Pro	Asp
				170					175					180
Ser	Pro	Glu	Tyr	Lys	Ala	Ala	Cys	Lys	Leu	Trp	Asp	Leu	Tyr	Leu
				185					190					195
Arg	Thr	Arg	Asn	Glu	Phe	Val	Gln	Lys	Gly	Glu	Ala	Asp	Asp	Glu
				200					205					210
Asp	Asp	Asp	Glu	Asp	Gly	Gln	Asp	Asn	Gln	Gly	Thr	Val	Thr	Glu
				215					220					225
Gly	Ser	Ser	Pro	Ala	Tyr	Leu	Lys	Glu	Ile	Leu	Glu	Gln	Leu	Leu
				230					235					240
Glu	Ala	Ile	Val	Val	Ala	Thr	Asn	Pro	Ser	Gly	Arg	Leu	Ile	Ser
				245					250					255
Glu	Leu	Phe	Gln	Lys	Leu	Pro	Ser	Lys	Val	Gln	Tyr	Pro	Asp	Tyr
				260					265					270
Tyr	Ala	Ile	Ile	Lys	Glu	Pro	Ile	Asp	Leu	Lys	Thr	Ile	Ala	Gln
				275					280					285
Arg	Ile	Gln	Asn	Gly	Ser	Tyr	Lys	Ser	Ile	His	Ala	Met	Ala	Lys
				290					295					300
Asp	Ile	Asp	Leu	Leu	Ala	Lys	Asn	Ala	Lys	Thr	Tyr	Asn	Glu	Pro
				305					310					315
Gly	Ser	Gln	Val	Phe	Lys	Asp	Ala	Asn	Ser	Ile	Lys	Lys	Ile	Phe
				320					325					330
Tyr	Met	Lys	Lys	Ala	Glu	Ile	Glu	His	His	Glu	Met	Ala	Lys	Ser
				335					340					345
Ser	Leu	Arg	Met	Arg	Thr	Pro	Ser	Asn	Leu	Ala	Ala	Ala	Arg	Leu
				350					355					360
Thr	Gly	Pro	Ser	His	Ser	Lys	Gly	Ser	Leu	Gly	Glu	Glu	Arg	Asn
				365					370					375
Pro	Thr	Ser	Lys	Tyr	Tyr	Arg	Asn	Lys	Arg	Ala	Val	Gln	Gly	Gly
				380					385					390
Arg	Leu	Ser	Ala	Ile	Thr	Met	Ala	Leu	Gln	Tyr	Gly	Ser	Glu	Ser
				395					400					405
Glu	Glu	Asp	Ala	Ala	Leu	Ala	Ala	Ala	Arg	Tyr	Glu	Glu	Gly	Glu
				410					415					420
Ser	Glu	Ala	Glu	Ser	Ile	Thr	Ser	Phe	Met	Asp	Val	Ser	Asn	Pro
				425					430					435
Phe	Tyr	Gln	Leu	Tyr	Asp	Thr	Val	Arg	Ser	Cys	Arg	Asn	Asn	Gln
				440					445					450
Gly	Gln	Leu	Ile	Ala	Glu	Pro	Phe	Tyr	His	Leu	Pro	Ser	Lys	Lys
				455					460					465
Lys	Tyr	Pro	Asp	Tyr	Tyr	Gln	Gln	Ile	Lys	Met	Pro	Ile	Ser	Leu
				470					475					480
Gln	Gln	Ile	Arg	Thr	Lys	Leu	Lys	Asn	Gln	Glu	Tyr	Glu	Thr	Leu
				485					490					495
Asp	His	Leu	Glu	Cys	Asp	Leu	Asn	Leu	Met	Phe	Glu	Asn	Ala	Lys
				500					505					510
Arg	Tyr	Asn	Val	Pro	Asn	Ser	Ala	Ile	Tyr	Lys	Arg	Val	Leu	Lys
				515					520					525
Leu	Gln	Gln	Val	Met	Gln	Ala	Lys	Lys	Lys	Glu	Leu	Ala	Arg	Arg
				530					535					540
Asp	Asp	Ile	Glu	Asp	Gly	Asp	Ser	Met	Ile	Ser	Ser	Ala	Thr	Ser

	545		550		555
Asp Thr Gly Ser	Ala Lys Arg Lys Ser	Lys Lys Asn Ile Arg	Lys		
	560		565		570
Gln Arg Met Lys	Ile Leu Phe Asn Val	Val Leu Glu Ala Arg	Glu		
	575		580		585
Pro Gly Ser Gly	Arg Arg Leu Cys Asp	Leu Phe Met Val Lys	Pro		
	590		595		600
Ser Lys Lys Asp	Tyr Pro Asp Tyr Tyr	Lys Ile Ile Leu Glu	Pro		
	605		610		615
Met Asp Leu Lys	Ile Ile Glu His Asn	Ile Arg Asn Asp Lys	Tyr		
	620		625		630
Ala Gly Glu Glu	Gly Met Ile Glu Asp	Met Lys Leu Met Phe	Arg		
	635		640		645
Asn Ala Arg His	Tyr Asn Glu Glu Gly	Ser Gln Val Tyr Asn	Asp		
	650		655		660
Ala His Ile Leu	Glu Lys Leu Leu Lys	Glu Lys Arg Lys Glu	Leu		
	665		670		675
Gly Pro Leu Pro	Asp Asp Asp Asp Met	Ala Ser Pro Lys Leu	Lys		
	680		685		690
Leu Ser Arg Lys	Ser Gly Ile Ser Pro	Lys Lys Ser Lys Tyr	Met		
	695		700		705
Thr Pro Met Gln	Gln Lys Leu Asn Glu	Val Tyr Glu Ala Val	Lys		
	710		715		720
Asn Tyr Thr Asp	Lys Arg Gly Arg Arg	Leu Ser Ala Ile Phe	Leu		
	725		730		735
Arg Leu Pro Ser	Arg Ser Glu Leu Pro	Asp Tyr Tyr Leu Thr	Ile		
	740		745		750
Lys Lys Pro Met	Asp Met Glu Lys Ile	Arg Ser His Met Met	Ala		
	755		760		765
Asn Lys Tyr Gln	Asp Ile Asp Ser Met	Val Glu Asp Phe Val	Met		
	770		775		780
Met Phe Asn Asn	Ala Cys Thr Tyr Asn	Glu Pro Glu Ser Leu	Ile		
	785		790		795
Tyr Lys Asp Ala	Leu Val Leu His Lys	Val Leu Leu Glu Thr	Arg		
	800		805		810
Arg Asp Leu Glu	Gly Asp Glu Asp Ser	His Val Pro Asn Val	Thr		
	815		820		825
Leu Leu Ile Gln	Glu Leu Ile His Asn	Leu Phe Val Ser Val	Met		
	830		835		840
Ser His Gln Asp	Asp Glu Gly Arg Cys	Tyr Ser Asp Ser Leu	Ala		
	845		850		855
Glu Ile Pro Ala	Val Asp Pro Asn Phe	Pro Asn Lys Pro Pro	Leu		
	860		865		870
Thr Phe Asp Ile	Ile Arg Lys Asn Val	Glu Asn Asn Arg Tyr	Arg		
	875		880		885
Arg Leu Asp Leu	Phe Gln Glu His Met	Phe Glu Val Leu Glu	Arg		
	890		895		900
Ala Arg Arg Met	Asn Arg Thr Asp Ser	Glu Ile Tyr Glu Asp	Ala		
	905		910		915
Val Glu Leu Gln	Gln Phe Phe Ile Lys	Ile Arg Asp Glu Leu	Cys		
	920		925		930
Lys Asn Gly Glu	Ile Leu Leu Ser Pro	Ala Leu Ser Tyr Thr	Thr		
	935		940		945
Lys His Leu His	Asn Asp Val Glu Lys	Glu Arg Lys Glu Lys	Leu		
	950		955		960
Pro Lys Glu Ile	Glu Glu Asp Lys Leu	Lys Arg Glu Glu Glu	Lys		
	965		970		975
Arg Glu Ala Glu	Lys Ser Glu Asp Ser	Ser Gly Ala Ala Gly	Leu		
	980		985		990
Ser Gly Leu His	Arg Thr Tyr Ser Gln	Asp Cys Ser Phe Lys	Asn		
	995		1000		1005
Ser Met Tyr His	Val Gly Asp Tyr Val	Tyr Val Glu Pro Ala	Glu		
	1010		1015		1020

Ala	Asn	Leu	Gln	Pro	His	Ile	Val	Cys	Ile	Glu	Arg	Leu	Trp	Glu	
				1025					1030					1035	
Asp	Ser	Ala	Gly	Glu	Lys	Trp	Leu	Tyr	Gly	Cys	Trp	Phe	Tyr	Arg	
				1040					1045					1050	
Pro	Asn	Glu	Thr	Phe	His	Leu	Ala	Thr	Arg	Lys	Phe	Leu	Glu	Lys	
				1055					1060					1065	
Glu	Val	Phe	Lys	Ser	Asp	Tyr	Tyr	Asn	Lys	Val	Pro	Val	Ser	Lys	
				1070					1075					1080	
Ile	Leu	Gly	Lys	Cys	Val	Val	Met	Phe	Val	Lys	Glu	Tyr	Phe	Lys	
				1085					1090					1095	
Leu	Cys	Pro	Glu	Asn	Phe	Arg	Asp	Glu	Asp	Val	Phe	Val	Cys	Glu	
				1100					1105					1110	
Ser	Arg	Tyr	Ser	Ala	Lys	Thr	Lys	Ser	Phe	Lys	Lys	Ile	Lys	Leu	
				1115					1120					1125	
Trp	Thr	Met	Pro	Ile	Ser	Ser	Val	Arg	Phe	Val	Pro	Arg	Asp	Val	
				1130					1135					1140	
Pro	Leu	Pro	Val	Val	Arg	Val	Ala	Ser	Val	Phe	Ala	Asn	Ala	Asp	
				1145					1150					1155	
Lys	Gly	Asp	Asp	Glu	Lys	Asn	Thr	Asp	Asn	Ser	Glu	Asp	Ser	Arg	
				1160					1165					1170	
Ala	Glu	Asp	Asn	Phe	Asn	Leu	Glu	Lys	Glu	Lys	Glu	Asp	Val	Pro	
				1175					1180					1185	
Val	Glu	Met	Ser	Asn	Gly	Glu	Pro	Gly	Cys	His	Tyr	Phe	Glu	Gln	
				1190					1195					1200	
Leu	His	Tyr	Asn	Asp	Met	Trp	Leu	Lys	Val	Gly	Asp	Cys	Val	Phe	
				1205					1210					1215	
Ile	Lys	Ser	His	Gly	Leu	Val	Arg	Pro	Arg	Val	Gly	Arg	Ile	Glu	
				1220					1225					1230	
Lys	Val	Trp	Val	Arg	Asp	Gly	Ala	Ala	Tyr	Phe	Tyr	Gly	Pro	Ile	
				1235					1240					1245	
Phe	Ile	His	Pro	Glu	Glu	Thr	Glu	His	Glu	Pro	Thr	Lys	Met	Phe	
				1250					1255					1260	
Tyr	Lys	Lys	Glu	Val	Phe	Leu	Ser	Asn	Leu	Glu	Glu	Thr	Cys	Pro	
				1265					1270					1275	
Met	Thr	Cys	Ile	Leu	Gly	Lys	Cys	Ala	Val	Leu	Ser	Phe	Lys	Asp	
				1280					1285					1290	
Phe	Leu	Ser	Cys	Arg	Pro	Thr	Glu	Ile	Pro	Glu	Asn	Asp	Ile	Leu	
				1295					1300					1305	
Leu	Cys	Glu	Ser	Arg	Tyr	Asn	Glu	Ser	Asp	Lys	Gln	Met	Lys	Lys	
				1310					1315					1320	
Phe	Lys	Gly	Leu	Lys	Arg	Phe	Ser	Leu	Ser	Ala	Lys	Val	Val	Asp	
				1325					1330					1335	
Asp	Glu	Ile	Tyr	Tyr	Phe	Arg	Lys	Pro	Ile	Val	Pro	Gln	Lys	Glu	
				1340					1345					1350	
Pro	Ser	Pro	Leu	Leu	Glu	Lys	Lys	Ile	Gln	Leu	Leu	Glu	Ala	Lys	
				1355					1360					1365	
Phe	Ala	Glu	Leu	Glu	Gly	Gly	Asp	Asp	Asp	Ile	Glu	Glu	Met	Gly	
				1370					1375					1380	
Glu	Glu	Asp	Ser	Glu	Val	Ile	Glu	Pro	Pro	Ser	Leu	Pro	Gln	Leu	
				1385					1390					1395	
Gln	Thr	Pro	Leu	Ala	Ser	Glu	Leu	Asp	Leu	Met	Pro	Tyr	Thr	Pro	
				1400					1405					1410	
Pro	Gln	Ser	Thr	Pro	Lys	Ser	Ala	Lys	Gly	Ser	Ala	Lys	Lys	Glu	
				1415					1420					1425	
Gly	Ser	Lys	Arg	Lys	Ile	Asn	Met	Ser	Gly	Tyr	Ile	Leu	Phe	Ser	
				1430					1435					1440	
Ser	Glu	Met	Arg	Ala	Val	Ile	Lys	Ala	Gln	His	Pro	Asp	Tyr	Ser	
				1445					1450					1455	
Phe	Gly	Glu	Leu	Ser	Arg	Leu	Val	Gly	Thr	Glu	Trp	Arg	Asn	Leu	
				1460					1465					1470	
Glu	Thr	Ala	Lys	Lys	Ala	Glu	Tyr	Glu	Gly	Val	Met	Asn	Gln	Gly	
				1475					1480					1485	
Val	Ala	Pro	Met	Val	Gly	Thr	Pro	Ala	Pro	Gly	Gly	Ser	Pro	Tyr	

1490	1495	1500
Gly Gln Gln Val Gly Val Leu Gly Pro Pro Gly Gln Gln Ala Pro		
1505	1510	1515
Pro Pro Tyr Pro Gly Pro His Pro Ala Gly Pro Pro Val Ile Gln		
1520	1525	1530
Gln Pro Thr Thr Pro Met Phe Val Ala Pro Pro Pro Lys Thr Gln		
1535	1540	1545
Arg Leu Leu His Ser Glu Ala Tyr Leu Lys Tyr Ile Glu Gly Leu		
1550	1555	1560
Ser Ala Glu Ser Asn Ser Ile Ser Lys Trp Asp Gln Thr Leu Ala		
1565	1570	1575
Ala Arg Arg Arg Asp Val His Leu Ser Lys Glu Gln Glu Ser Arg		
1580	1585	1590
Leu Pro Ser His Trp Leu Lys Ser Lys Gly Ala His Thr Thr Met		
1595	1600	1605
Ala Asp Ala Leu Trp Arg Leu Arg Asp Leu Met Leu Arg Asp Thr		
1610	1615	1620
Leu Asn Ile Arg Gln Ala Tyr Asn Leu Glu Asn Val		
1625	1630	

&lt;210&gt; 149

&lt;211&gt; 736

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:236767.26.orf2:2002JAN18

&lt;400&gt; 149

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Pro Pro Leu Ser Pro Lys Ser Gly Ala Glu Val Glu Ala Gly Asp	10
20	25
Ala Ala Glu Arg Arg Ala Pro Glu Glu Glu Leu Pro Pro Leu Asp	30
35	40
Pro Glu Glu Ile Arg Lys Arg Leu Glu His Thr Glu Arg Gln Phe	45
50	55
Arg Asn Arg Arg Lys Ile Leu Ile Arg Gly Leu Pro Gly Asp Val	60
65	70
Thr Asn Gln Glu Val His Asp Leu Leu Ser Asp Tyr Glu Leu Lys	75
80	85
Tyr Cys Phe Val Asp Lys Tyr Lys Gly Thr Ala Phe Val Thr Leu	90
95	100
Leu Asn Gly Glu Gln Ala Glu Ala Ala Ile Asn Ala Phe His Gln	105
110	115
Ser Arg Leu Arg Glu Arg Glu Leu Ser Val Gln Leu Gln Pro Thr	120
125	130
Asp Ala Leu Leu Cys Val Ala Asn Leu Pro Pro Ser Leu Thr Gln	135
140	145
Gln Gln Phe Glu Glu Leu Val Arg Pro Phe Gly Ser Leu Glu Arg	150
155	160
Cys Phe Leu Val Tyr Ser Glu Arg Thr Gly Gln Ser Lys Gly Tyr	165
170	175
Gly Phe Ala Glu Tyr Met Lys Lys Asp Ser Ala Ala Arg Ala Lys	180
185	190
Ser Asp Leu Leu Gly Lys Pro Leu Gly Pro Arg Thr Leu Tyr Val	195
200	205
His Trp Thr Asp Ala Gly Gln Leu Thr Pro Ala Leu Leu His Ser	210
215	220
Arg Cys Leu Cys Val Asp Arg Leu Pro Pro Gly Phe Asn Asp Val	225
230	235
Asp Ala Leu Cys Arg Ala Leu Ser Ala Val His Ser Pro Thr Phe	240

	245		250		255
Cys Gln Leu Ala	Cys Gly Gln Asp Gly	Gln Leu Lys Gly Phe	Ala		
	260		265		270
Val Leu Glu Tyr	Glu Thr Ala Glu Met	Ala Glu Glu Ala Gln	Gln		
	275		280		285
Gln Ala Asp Gly	Leu Ser Leu Gly Gly	Ser His Leu Arg Val	Ser		
	290		295		300
Phe Cys Ala Pro	Gly Pro Pro Gly Arg	Ser Met Leu Ala Ala	Leu		
	305		310		315
Ile Ala Ala Gln	Ala Thr Ala Leu Asn	Arg Gly Lys Gly Leu	Leu		
	320		325		330
Pro Glu Pro Asn	Ile Leu Gln Leu Leu	Asn Asn Leu Gly Pro	Ser		
	335		340		345
Ala Ser Leu Gln	Leu Leu Leu Asn Pro	Leu Leu His Gly Ser	Ala		
	350		355		360
Gly Gly Lys Gln	Gly Leu Leu Gly Ala	Pro Pro Ala Met Pro	Leu		
	365		370		375
Leu Asn Gly Pro	Ala Leu Ser Thr Ala	Leu Leu Gln Leu Ala	Leu		
	380		385		390
Gln Thr Gln Gly	Gln Lys Lys Pro Gly	Ile Leu Gly Asp Ser	Pro		
	395		400		405
Leu Gly Ala Leu	Gln Pro Gly Ala Gln	Pro Ala Asn Pro Leu	Leu		
	410		415		420
Gly Glu Leu Pro	Ala Gly Gly Gly Leu	Pro Pro Glu Leu Pro	Pro		
	425		430		435
Arg Arg Gly Lys	Pro Pro Pro Leu Leu	Pro Ser Val Leu Gly	Pro		
	440		445		450
Ala Gly Gly Asp	Arg Glu Ala Leu Gly	Leu Gly Pro Pro Ala	Ala		
	455		460		465
Gln Leu Thr Pro	Pro Pro Ala Pro Val	Gly Leu Arg Gly Ser	Gly		
	470		475		480
Leu Arg Gly Leu	Gln Lys Asp Ser Gly	Pro Leu Pro Thr Pro	Pro		
	485		490		495
Gly Val Ser Leu	Leu Gly Glu Pro Pro	Lys Asp Tyr Arg Ile	Pro		
	500		505		510
Leu Asn Pro Tyr	Leu Asn Leu His Ser	Leu Leu Pro Ala Ser	Asn		
	515		520		525
Leu Ala Gly Lys	Glu Ala Arg Gly Trp	Gly Gly Ala Gly Arg	Ser		
	530		535		540
Arg Arg Pro Ala	Glu Gly Pro Pro Thr	Asn Pro Pro Ala Pro	Gly		
	545		550		555
Gly Gly Ser Ser	Ser Ser Lys Ala Phe	Gln Leu Lys Ser Arg	Leu		
	560		565		570
Leu Ser Pro Leu	Ser Ser Ala Arg Leu	Pro Pro Glu Pro Gly	Leu		
	575		580		585
Ser Asp Ser Tyr	Ser Phe Asp Tyr Pro	Ser Asp Met Gly Pro	Arg		
	590		595		600
Arg Leu Phe Ser	His Pro Arg Glu Pro	Ala Leu Gly Pro His	Gly		
	605		610		615
Pro Ser Arg His	Lys Met Ser Pro Pro	Pro Ser Gly Phe Gly	Glu		
	620		625		630
Arg Ser Ser Gly	Gly Ser Gly Gly Gly	Pro Leu Ser His Phe	Tyr		
	635		640		645
Ser Gly Ser Pro	Thr Ser Tyr Phe Thr	Ser Gly Leu Gln Ala	Gly		
	650		655		660
Leu Lys Gln Ser	His Leu Ser Lys Ala	Ile Gly Ser Ser Pro	Leu		
	665		670		675
Gly Ser Gly Glu	Gly Leu Leu Gly Leu	Ser Pro Gly Pro Asn	Gly		
	680		685		690
His Ser His Leu	Leu Lys Thr Pro Leu	Gly Gly Arg Asn Ala	Ala		
	695		700		705
Leu Pro Thr Cys	Cys Pro Arg Pro Ser	Pro Ala Gln Lys Ala	Ala		
	710		715		720



Met Trp Ala Ser Thr Pro Arg Pro Arg Arg His Tyr Ala Asp Ser  
 725 730 735

Thr

<210> 150  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:237489.7.orf1:2002JAN18

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 Leu Lys Glu Val Val Phe Ser Pro Gly Leu Leu Leu Thr Ser Leu  
 20 25 30  
 Phe Ser Gln Cys Ile Trp Val Val Ser Phe Leu Ser Ser Phe Phe  
 35 40 45  
 Leu Ser Leu Pro Tyr Gly Val Ala Val Gly Val Ala Phe Ser Val  
 50 55 60  
 Leu Val Val Val Phe Gln Thr Gln Phe Arg Asn Gly Tyr Ala Leu  
 65 70 75  
 Ala Gln Val Met Asp Thr Asp Ile Tyr Val Asn Pro Lys Thr Tyr  
 80 85 90  
 Asn Arg Ala Gln Asp Ile Gln Gly Ile Lys Ile Ile Thr Tyr Cys  
 95 100 105  
 Ser Pro Leu Tyr Phe Ala Asn Ser Glu Ile Phe Arg Gln Lys Val  
 110 115 120  
 Ile Ala Lys Thr Val Ser Leu Gln Glu Leu Gln Gln Asp Phe Glu  
 125 130 135  
 Asn Ala Pro Pro Thr Asp Pro Asn Asn Asn Gln Thr Pro Ala Asn  
 140 145 150  
 Gly Thr Ser Val Ser Tyr Ile Thr Phe Ser Pro Asp Ser Ser Ser  
 155 160 165  
 Pro Ala Gln Ser Glu Pro Pro Ala Ser Ala Glu Ala Pro Gly Glu  
 170 175 180  
 Pro Ser Asp Met Leu Ala Ser Val Pro Pro Phe Val Thr Phe His  
 185 190 195  
 Thr Leu Ile Leu Asp Met Ser Gly Val Ser Phe Val Asp Leu Met  
 200 205 210  
 Gly Ile Lys Ala Leu Ala Lys Leu Ser Ser Thr Tyr Gly Lys Ile  
 215 220 225  
 Gly Val Lys Val Phe Leu Val Asn Ile His Ala Gln Val Tyr Asn  
 230 235 240  
 Asp Ile Ser His Gly Gly Val Phe Glu Asp Gly Ser Leu Glu Cys  
 245 250 255  
 Lys His Val Phe Pro Ser Ile His Asp Ala Val Leu Phe Ala Gln  
 260 265 270  
 Ala Asn Ala Arg Asp Val Thr Pro Gly His Asn Phe Gln Gly Ala  
 275 280 285  
 Pro Gly Asp Ala Glu Leu Ser Leu Tyr Asp Ser Glu Glu Asp Ile  
 290 295 300  
 Arg Ser Tyr Trp Asp Leu Glu Gln Glu Met Phe Gly Ser Met Phe  
 305 310 315  
 His Ala Glu Thr Leu Thr Ala Leu  
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 <212> PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:238218.20.orf1:2002JAN18

&lt;400&gt; 151

Arg	Gly	Ala	Ala	Arg	Thr	Gly	Gly	Arg	Arg	Gly	Gly	Lys	Asp	Gly
1				5					10					15
Ala	Val	Thr	Ala	Gly	Pro	Glu	Pro	Ser	Arg	Pro	His	Pro	Ala	Pro
				20					25					30
Trp	Pro	Leu	Gly	Pro	Ala	Glu	Met	Glu	Ser	Thr	Ala	Tyr	Pro	Leu
				35					40					45
Asn	Leu	Ser	Leu	Lys	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Ile	Gln	Ser
				50					55					60
Arg	Glu	Leu	Glu	Asp	Gly	Pro	Ala	Asp	Met	Gln	Lys	Val	Arg	Ile
				65					70					75
Cys	Ser	Glu	Gly	Gly	Trp	Val	Pro	Ala	Leu	Phe	Asp	Glu	Val	Ala
				80					85					90
Ile	Tyr	Phe	Ser	Asp	Glu	Glu	Trp	Glu	Val	Leu	Thr	Glu	Gln	Gln
				95					100					105
Lys	Ala	Leu	Tyr	Arg	Glu	Val	Met	Arg	Met	Asn	Tyr	Glu	Thr	Val
				110					115					120
Leu	Ser	Leu	Glu	Phe	Pro	Phe	Pro	Lys	Pro	Asp	Met	Ile	Thr	Arg
				125					130					135
Leu	Glu	Gly	Glu	Glu	Glu	Ser	Gln	Asn	Ser	Asp	Glu	Trp	Gln	Leu
				140					145					150
Gln	Gly	Gly	Thr	Ser	Ala	Glu	Asn	Glu	Glu	Ser	Asp	Val	Lys	Pro
				155					160					165
Pro	Asp	Trp	Pro	Asn	Pro	Met	Asn	Ala	Thr	Ser	Gln	Phe	Pro	Gln
				170					175					180
Pro	Gln	His	Phe	Asp	Ser	Phe	Gly	Leu	Arg	Leu	Pro	Arg	Asp	Ile
				185					190					195
Thr	Glu	Leu	Pro	Glu	Trp	Ser	Glu	Gly	Tyr	Pro	Phe	Tyr	Met	Ala
				200					205					210
Met	Gly	Phe	Pro	Gly	Tyr	Asp	Leu	Ser	Ala	Asp	Asp	Ile	Ala	Gly
				215					220					225
Lys	Phe	Gln	Phe	Ser	Arg	Gly	Met	Arg	Arg	Ser	Tyr	Asp	Ala	Gly
				230					235					240
Phe	Lys	Leu	Met	Val	Val	Glu	Tyr	Ala	Glu	Ser	Thr	Asn	Asn	Cys
				245					250					255
Gln	Ala	Ala	Lys	Gln	Phe	Gly	Val	Leu	Glu	Lys	Asn	Val	Arg	Asp
				260					265					270
Trp	Arg	Lys	Val	Lys	Pro	Gln	Leu	Gln	Asn	Ala	His	Ala	Met	Arg
				275					280					285
Arg	Ala	Phe	Arg	Gly	Pro	Lys	Asn	Gly	Arg	Phe	Ala	Leu	Val	Asp
				290					295					300
Gln	Arg	Val	Ala	Glu	Tyr	Val	Arg	Tyr	Met	Gln	Ala	Lys	Gly	Asp
				305					310					315
Pro	Ile	Thr	Arg	Glu	Ala	Met	Gln	Leu	Lys	Ala	Leu	Glu	Ile	Ala
				320					325					330
Gln	Glu	Met	Asn	Ile	Pro	Glu	Lys	Gly	Phe	Lys	Ala	Ser	Leu	Gly
				335					340					345
Trp	Cys	Arg	Arg	Met	Met	Arg	Arg	Tyr	Asp	Leu	Ser	Leu	Arg	His
				350					355					360
Lys	Val	Pro	Val	Pro	Gln	His	Leu	Pro	Glu	Asp	Leu	Thr	Glu	Lys
				365					370					375
Leu	Val	Thr	Tyr	Gln	Arg	Ser	Val	Leu	Ala	Leu	Arg	Arg	Ala	His
				380					385					390
Asp	Tyr	Glu	Val	Ala	Gln	Met	Gly	Asn	Ala	Asp	Glu	Thr	Pro	Ile
				395					400					405
Cys	Leu	Glu	Val	Pro	Ser	Arg	Val	Thr	Val	Asp	Asn	Gln	Gly	Glu
				410					415					420

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Lys	Pro	Val	Leu	Ala	Asp	Gly	Arg	Lys	Leu	Pro	Pro	Tyr	Ile	Ile	425	430	435
Leu	Arg	Gly	Thr	Tyr	Ile	Pro	Pro	Gly	Lys	Phe	Pro	Ser	Gly	Met	440	445	450
Glu	Ile	Arg	Cys	His	Arg	Tyr	Gly	Trp	Met	Thr	Glu	Asp	Leu	Met	455	460	465
Gln	Asp	Trp	Leu	Glu	Val	Val	Trp	Arg	Arg	Arg	Thr	Gly	Ala	Val	470	475	480
Pro	Lys	Gln	Arg	Gly	Met	Leu	Ile	Leu	Asn	Gly	Phe	Arg	Gly	His	485	490	495
Gly	Lys	Asp	Ser	Val	Lys	Asn	Ser	Met	Glu	Ser	Met	Asn	Thr	Asp	500	505	510
Met	Val	Ile	Ile	Pro	Gly	Gly	Leu	Thr	Ser	Gln	Leu	Gln	Val	Leu	515	520	525
Asp	Val	Val	Val	Tyr	Lys	Pro	Leu	Asn	Asp	Ser	Val	Arg	Ala	Gln	530	535	540
Tyr	Ser	Asn	Trp	Leu	Leu	Ala	Gly	Asn	Leu	Ala	Leu	Ser	Pro	Thr	545	550	555
Gly	Asn	Ala	Lys	Lys	Pro	Pro	Leu	Gly	Leu	Phe	Leu	Glu	Trp	Val	560	565	570
Met	Val	Ala	Trp	Asn	Ser	Ile	Ser	Ser	Glu	Ser	Ile	Val	Gln	Gly	575	580	585
Phe	Lys	Lys	Cys	His	Ile	Ser	Ser	Asn	Leu	Glu	Glu	Glu	Asp	Asp	590	595	600
Val	Leu	Trp	Glu	Ile	Glu	Ser	Glu	Leu	Pro	Gly	Gly	Gly	Glu	Pro	605	610	615
Pro	Lys	Asp	Cys	Asp	Thr	Glu	Ser	Met	Ala	Glu	Ser	Asn			620	625	

&lt;210&gt; 152

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:239939.14.orf3:2002JAN18

&lt;400&gt; 152

His	Arg	Lys	Asp	Gly	Val	Val	Glu	Arg	Gly	Leu	Glu	Glu	Trp	Arg	1	5	10	15
Asn	Lys	Gly	Lys	Thr	Ser	Leu	Ala	His	Gln	Phe	Val	Glu	Gly	Glu	20	25	30	35
Phe	Ser	Glu	Gly	Tyr	Asp	Pro	Thr	Val	Glu	Asn	Thr	Tyr	Ser	Lys	40	45	50	55
Ile	Val	Thr	Leu	Gly	Lys	Asp	Glu	Phe	His	Leu	His	Leu	Val	Asp	60	65	70	75
Thr	Ala	Gly	Gln	Asp	Glu	Tyr	Ser	Ile	Leu	Pro	Tyr	Ser	Phe	Ile	80	85	90	95
Ile	Gly	Val	His	Gly	Tyr	Val	Leu	Val	Tyr	Ser	Val	Thr	Ser	Leu	100	105	110	115
His	Ser	Phe	Gln	Val	Ile	Glu	Ser	Leu	Tyr	Gln	Lys	Leu	His	Glu	120	125	130	135
Gly	His	Gly	Lys	Thr	Arg	Val	Pro	Val	Val	Leu	Val	Gly	Asn	Lys	140	145	150	155
Ala	Asp	Leu	Ser	Pro	Glu	Arg	Glu	Val	Gln	Ala	Val	Glu	Gly	Lys	160	165	170	175
Lys	Leu	Ala	Glu	Ser	Trp	Gly	Ala	Thr	Phe	Met	Glu	Ser	Ser	Ala				
Arg	Glu	Asn	Gln	Leu	Thr	Gln	Gly	Ile	Phe	Thr	Lys	Val	Ile	Gln				
Glu	Ile	Ala	Arg	Val	Glu	Asn	Ser	Tyr	Gly	Gln	Glu	Arg	Arg	Cys				

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<210> 153
<211> 338
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:242288.11.orf1:2002JAN18
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<210>	154
<211>	191
<212>	PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:242491.29.orf1:2002JAN18

&lt;400&gt; 154

```

Gly Ala Met Ala Gly Val Gly Ala Gly Pro Leu Arg Ala Met Gly
1      5      10      15
Arg Gln Ala Leu Leu Leu Ala Leu Cys Ala Thr Gly Ala Gln
20      25      30
Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys Arg Cys Phe Ile
35      40      45
Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn Tyr Arg Thr
50      55      60
Gln Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser Thr Pro
65      70      75
Gly Leu Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys Met
80      85      90
Leu Gln Val Val Leu Ser Arg Gln Tyr Gly Ser Glu Gly Arg Phe
95      100      105
Thr Phe Thr Ser His Thr Pro Gly Asp His Gln Ile Cys Leu His
110      115      120
Ser Asn Ser Thr Arg Met Ala Leu Phe Ala Gly Gly Lys Leu Arg
125      130      135
Val His Leu Asp Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro
140      145      150
Glu Ile Ala Ala Lys Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala
155      160      165
Arg Gln Leu Leu Asp Gln Val Glu Gln Ile Gln Lys Glu Gln Asp
170      175      180
Tyr Gln Arg Ala Ser Ala Tyr Leu Leu Val Ile
185      190

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&lt;210&gt; 155

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:243488.41.orf3:2002JAN18

&lt;400&gt; 155

```

Ala Ala Ala Val Ala Phe Gly Ala Glu Val Gly Val Arg Leu Ala
1      5      10      15
Leu Phe Ala Ala Phe Leu Val Thr Glu Leu Leu Pro Pro Phe Gln
20      25      30
Arg Leu Ile Gln Pro Glu Glu Met Trp Leu Tyr Arg Asn Pro Tyr
35      40      45
Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Lys Ala Asp
50      55      60
Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu Ala Leu
65      70      75
Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val Gly
80      85      90
Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu
95      100      105
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn
110      115      120
Glu Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe
125      130      135
Ala Gly Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His

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Cys Phe Thr Pro	140	Gln Gly Arg Gly Lys	145	Ser Trp Arg Phe Cys	150
	155		160		165
Phe Leu Ser Pro	170	Leu Leu Phe Ala Ala	175	Val Ile Ala Leu Ser	180
	185		190		195
Thr Cys Asp Tyr	200	Lys His His Trp Gln	205	Asp Val Leu Val Gly	210
	215		220		225
Met Ile Gly Met	230	Thr Phe Ala Tyr Val	235	Cys Tyr Arg Gln Tyr	240
	245		250		255
Pro Pro Leu Thr	260	Asp Ala Glu Cys His	265	Lys Pro Phe Gln Asp	270
	275		280		285
Leu Val Leu Ser	290	Thr Ala Gln Lys Pro	295	Gly Asp Ser Tyr Cys	300
	305		310		315
Asp Asn Leu Lys		Ile Glu Ser Gly Arg		Ala Trp Trp Leu Met	
Val Ile Pro Thr		Leu Trp Glu Ala Glu		Glu Gly Gly Ser Pro	
Val Arg Thr Ser		Leu Ala Asn Met Val		Asn Pro Val Ser Thr	
Asn Thr Lys Ile		Ser Gln Glu Leu Cys		Ala Val Ile Pro Ala	
Trp Glu Ala Glu		Val Gly Glu Leu Leu		Glu Pro Gly Ser Trp	
Phe Gln					

&lt;210&gt; 156

&lt;211&gt; 617

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:247792.18.orf2:2002JAN18

&lt;400&gt; 156

Ser Leu Lys Trp Gly	1	Ser Gly Gly Arg Glu	5	Thr Ala Ser Arg Gly	15
	10		20		30
Ala Trp Lys Val Val	25	Lys Pro Glu Ser Asn	35	Asp Lys Glu Thr Glu	45
	40		50		60
Ala Ala Tyr Glu Ser	55	Asp Ile Pro Glu Glu	65	Leu Cys Gly His His	75
	70		80		90
Leu Pro Gln Gln Ser	85	Leu Lys Ser Tyr Asn	95	Asp Ser Pro Asp Val	105
	100		110		120
Ile Val Glu Ala Gln	115	Phe Asp Gly Ser Asp	125	Ser Glu Asp Gly His	135
	130		140		150
Gly Ile Thr Gln Asn	145	Val Leu Val Asp Gly	155	Val Lys Lys Leu Ser	
	160		170		
Val Cys Val Ser Glu	175	Lys Gly Arg Glu Asp	185	Gly Asp Ala Pro Val	
	190		200		
Thr Lys Asp Glu Thr	205	Thr Cys Ile Ser Gln	215	Asp Thr Arg Ala Leu	
	220		230		
Ser Glu Lys Ser Leu	235	Gln Arg Ser Ala Lys	245	Val Val Tyr Ile Leu	
	250		260		
Glu Lys Lys His Ser	265	Arg Ala Ala Thr Gly	275	Phe Leu Lys Leu Leu	
	280		290		
Ala Asp Lys Asn Ser	295	Glu Leu Phe Arg Lys	305	Tyr Ala Leu Phe Ser	
	310		320		
Pro Ser Asp His Arg	325	Val Pro Arg Ile Tyr	335	Val Pro Leu Lys Asp	
	340		350		
Cys Pro Gln Asp Phe	355	Val Ala Arg Pro Lys	365	Asp Tyr Ala Asn Thr	
	370		380		
Leu Phe Ile Cys Arg	385	Ile Val Asp Trp Lys	395	Glu Asp Cys Asn Phe	

Ala Leu Gly Gln	200	Ala Lys Ser Leu	205	Gln Ala Gly Glu	210
	215		220		225
Glu Pro Glu Thr	230	Glu Gly Ile Leu Thr	235	Glu Tyr Gly Val Asp	240
	245		250		255
Ser Asp Phe Ser	260	Ser Glu Val Leu Glu	265	Cys Leu Pro Gln Gly	270
	275		280		285
Pro Trp Thr Ile	290	Pro Pro Glu Glu Phe	295	Ser Lys Arg Arg Asp	300
	305		310		315
Arg Lys Asp Cys	320	Ile Phe Thr Ile Asp	325	Pro Ser Thr Ala Arg	330
	335		340		345
Leu Asp Asp Ala	350	Leu Ser Cys Lys Pro	355	Leu Ala Asp Gly Asn	360
	365		370		375
Lys Val Gly Val	380	His Ile Ala Asp Val	385	Ser Tyr Phe Val Pro	390
	395		400		405
Gly Ser Asp Leu	410	Asp Lys Val Ala Ala	415	Glu Arg Ala Thr Ser	420
	425		430		435
Tyr Leu Val Gln	440	Lys Val Val Pro Met	445	Leu Pro Arg Leu Leu	450
	455		460		465
Glu Glu Leu Cys	470	Ser Leu Asn Pro Met	475	Ser Asp Lys Leu Thr	480
	485		490		495
Ser Val Ile Trp	500	Thr Leu Thr Pro Glu	505	Gly Lys Ile Leu Asp	510
	515		520		525
Trp Phe Gly Arg	530	Thr Ile Ile Arg Ser	535	Cys Thr Lys Leu Ser	540
	545		550		555
Glu His Ala Gln	560	Ser Met Ile Glu Ser	565	Pro Thr Glu Lys Ile	570
	575		580		585
Ala Lys Glu Leu	590	Pro Pro Ile Ser Pro	595	Glu His Ser Ser Glu	600
	605		610		615
Val His Gln Ala		Val Leu Asn Leu His		Gly Ile Ala Lys Gln	
Arg Gln Gln Arg		Phe Val Asp Gly Ala		Leu Arg Leu Asp Gln	
Lys Leu Ala Phe		Thr Leu Asp His Glu		Thr Gly Leu Pro Gln	
Cys His Ile Tyr		Glu Tyr Arg Glu Ser		Asn Lys Leu Val Glu	
Phe Met Leu Leu		Ala Asn Met Ala Val		Ala His Lys Ile His	
Ala Phe Pro Glu		Gln Ala Leu Leu Arg		Arg His Pro Pro Pro	
Thr Arg Met Leu		Ser Asp Leu Val Glu		Phe Cys Asp Gln Met	
Leu Pro Val Asp		Phe Ser Ser Ala Gly		Ala Leu Asn Lys Ser	
Thr Gln Thr Phe		Gly Asp Asp Lys Tyr		Ser Leu Ala Arg Lys	
Val Leu Thr Asn		Met Cys Ser Arg Pro		Met Gln Met Ala Leu	
Phe Cys Ser Gly		Leu Leu Gln Asp Pro		Ala Gln Phe Arg His	
Ala Leu Asn Val		Pro Ser Val His Thr		Leu His Leu Ala His	
Pro Leu Cys Arg		Arg Pro Gly Ala Pro		Pro Pro Gly Cys Arg	
Arg Leu					

&lt;210&gt; 157

&lt;211&gt; 371

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:253193.17.orf3:2002JAN18

&lt;400&gt; 157

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Tyr Leu Asn Leu Leu Val Thr Ser Trp Arg Met Asn Asp Ser Leu
  1          5          10          15
Val Ile Gln Gln Asn Asp Leu Val Phe Glu Phe Ala Ser Asn Val
          20          25          30
Met Glu Asp Glu Arg Gln Leu Gly Asp Pro Ala Ile Phe Pro Ala
          35          40          45
Val Ile Val Glu His Val Pro Gly Ala Asp Ile Leu Asn Ser Tyr
          50          55          60
Ala Gly Leu Ala Cys Val Glu Glu Pro Asn Asp Met Ile Thr Glu
          65          70          75
Ser Ser Leu Asp Val Ala Glu Glu Glu Ile Ile Asp Asp Asp Asp
          80          85          90
Asp Asp Ile Thr Leu Thr Val Glu Ala Ser Cys His Asp Gly Asp
          95          100          105
Glu Thr Ile Glu Thr Ile Glu Ala Ala Glu Ala Leu Leu Asn Met
          110          115          120
Asp Ser Pro Gly Pro Met Leu Asp Glu Lys Arg Ile Asn Asn Asn
          125          130          135
Ile Phe Ser Ser Pro Glu Asp Asp Met Val Val Ala Pro Val Thr
          140          145          150
His Val Ser Val Thr Leu Asp Gly Ile Pro Glu Val Met Glu Thr
          155          160          165
Gln Gln Val Gln Glu Lys Tyr Ala Asp Ser Pro Gly Ala Ser Ser
          170          175          180
Pro Glu Gln Pro Lys Arg Lys Lys Gly Arg Lys Thr Lys Pro Pro
          185          190          195
Arg Pro Asp Ser Pro Ala Thr Thr Pro Asn Ile Ser Val Lys Lys
          200          205          210
Lys Asn Lys Asp Gly Lys Gly Asn Thr Ile Tyr Leu Trp Glu Phe
          215          220          225
Leu Leu Ala Leu Leu Gln Asp Lys Ala Thr Cys Pro Lys Tyr Ile
          230          235          240
Lys Trp Thr Gln Arg Glu Lys Gly Ile Phe Lys Leu Val Asp Ser
          245          250          255
Lys Ala Val Ser Arg Leu Trp Gly Lys His Lys Asn Lys Pro Asp
          260          265          270
Met Asn Tyr Glu Thr Met Gly Arg Ala Leu Arg Tyr Tyr Tyr Gln
          275          280          285
Arg Gly Ile Leu Ala Lys Val Glu Gly Gln Arg Leu Val Tyr Gln
          290          295          300
Phe Lys Glu Met Pro Lys Asp Leu Ile Tyr Ile Asn Asp Glu Asp
          305          310          315
Pro Ser Ser Ser Ile Glu Ser Ser Asp Pro Ser Leu Ser Ser Ser
          320          325          330
Ala Thr Ser Asn Arg Asn Gln Thr Ser Arg Ser Arg Val Ser Ser
          335          340          345
Ser Pro Gly Val Lys Gly Gly Ala Thr Thr Val Leu Lys Pro Gly
          350          355          360
Asn Ser Lys Ser Cys Lys Ser Gln Arg Ser Cys
          365          370

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&lt;210&gt; 158

&lt;211&gt; 871

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature



&lt;223&gt; Incyte ID No: LG:257088.20.orf2:2002JAN18

&lt;400&gt; 158

Arg	Leu	Phe	Val	Leu	Ile	Ser	Leu	Glu	Leu	Lys	Met	Leu	Tyr	Phe
1				5					10					15
Ser	Arg	Ser	His	Phe	Pro	Arg	Pro	Cys	Gly	Gly	Gln	Val	Ser	Ala
				20					25					30
Gly	Ser	Gly	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Pro	Ala	Leu	Trp	
				35					40					45
Arg	Gly	Trp	Leu	Glu	Gly	Asp	Gly	Gln	Gln	Ala	Val	Pro	Ala	Arg
				50					55					60
Gly	Glu	Pro	Gln	Gln	Asp	Cys	Cys	Val	Lys	Thr	Glu	Leu	Leu	Gly
				65					70					75
Glu	Glu	Thr	Pro	Met	Ala	Ala	Asp	Glu	Gly	Ser	Ala	Glu	Lys	Gln
				80					85					90
Ala	Gly	Glu	Ala	His	Met	Ala	Ala	Asp	Gly	Glu	Thr	Asn	Gly	Ser
				95					100					105
Cys	Glu	Asn	Ser	Asp	Ala	Ser	Ser	His	Ala	Asn	Ala	Ala	Lys	His
				110					115					120
Thr	Gln	Asp	Ser	Ala	Arg	Val	Asn	Pro	Gln	Asp	Gly	Thr	Asn	Thr
				125					130					135
Leu	Thr	Arg	Ile	Ala	Glu	Asn	Gly	Val	Ser	Glu	Arg	Asp	Ser	Glu
				140					145					150
Ala	Ala	Lys	Gln	Asn	His	Val	Thr	Ala	Asp	Asp	Phe	Val	Gln	Thr
				155					160					165
Ser	Val	Ile	Gly	Ser	Asn	Gly	Tyr	Ile	Leu	Asn	Lys	Pro	Ala	Leu
				170					175					180
Gln	Ala	Gln	Pro	Leu	Arg	Thr	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Leu
				185					190					195
Pro	Gly	His	Ala	Ala	Lys	Thr	Leu	Pro	Gly	Gly	Ala	Gly	Lys	Gly
				200					205					210
Arg	Thr	Pro	Ser	Ala	Phe	Pro	Gln	Thr	Pro	Ala	Ala	Pro	Pro	Ala
				215					220					225
Thr	Leu	Gly	Glu	Gly	Ser	Ala	Asp	Thr	Glu	Asp	Arg	Lys	Leu	Pro
				230					235					240
Ala	Pro	Gly	Ala	Asp	Val	Lys	Val	His	Arg	Ala	Arg	Lys	Thr	Met
				245					250					255
Pro	Lys	Ser	Val	Val	Gly	Leu	His	Ala	Ala	Ser	Lys	Asp	Pro	Arg
				260					265					270
Glu	Val	Arg	Glu	Ala	Arg	Asp	His	Lys	Glu	Pro	Lys	Glu	Glu	Ile
				275					280					285
Asn	Lys	Asn	Ile	Ser	Asp	Phe	Gly	Arg	Gln	Gln	Leu	Leu	Pro	Pro
				290					295					300
Phe	Pro	Ser	Leu	His	Gln	Ser	Leu	Pro	Gln	Asn	Gln	Cys	Tyr	Met
				305					310					315
Ala	Thr	Thr	Lys	Ser	Gln	Thr	Ala	Cys	Leu	Pro	Phe	Val	Leu	Ala
				320					325					330
Ala	Ala	Val	Ser	Arg	Lys	Lys	Lys	Arg	Arg	Met	Gly	Thr	Tyr	Ser
				335					340					345
Leu	Val	Pro	Lys	Lys	Lys	Thr	Lys	Val	Leu	Lys	Gln	Arg	Thr	Val
				350					355					360
Ile	Glu	Met	Phe	Lys	Ser	Ile	Thr	His	Ser	Thr	Val	Gly	Ser	Lys
				365					370					375
Gly	Glu	Lys	Asp	Leu	Gly	Ala	Ser	Ser	Leu	His	Val	Asn	Gly	Glu
				380					385					390
Ser	Leu	Glu	Met	Asp	Ser	Asp	Glu	Asp	Asp	Ser	Glu	Glu	Leu	Glu
				395					400					405
Glu	Asp	Asp	Gly	His	Gly	Ala	Glu	Gln	Ala	Ala	Ala	Phe	Pro	Thr
				410					415					420
Glu	Asp	Ser	Arg	Thr	Ser	Lys	Glu	Ser	Met	Ser	Glu	Ala	Asp	Arg
				425					430					435
Ala	Gln	Lys	Ser	Ser	Glu	Ser	Ser	Ile	Lys	Lys	Lys	Phe	Leu	Lys
				440					445					450

Arg	Lys	Gly	Lys	Thr	Asp	Ser	Pro	Trp	Ile	Lys	Pro	Ala	Arg	Lys
				455					460					465
Arg	Arg	Arg	Arg	Ser	Arg	Lys	Lys	Pro	Ser	Gly	Ala	Leu	Gly	Ser
				470					475					480
Glu	Ser	Tyr	Lys	Ser	Ser	Ala	Gly	Ser	Ala	Glu	Gln	Thr	Ala	Pro
				485					490					495
Gly	Asp	Ser	Thr	Gly	Tyr	Met	Glu	Val	Ser	Leu	Asp	Ser	Leu	Asp
				500					505					510
Leu	Arg	Val	Lys	Gly	Ile	Leu	Ser	Ser	Gln	Ala	Glu	Gly	Leu	Ala
				515					520					525
Asn	Gly	Pro	Asp	Val	Leu	Glu	Thr	Asp	Gly	Leu	Gln	Glu	Val	Pro
				530					535					540
Leu	Cys	Ser	Cys	Arg	Met	Glu	Thr	Pro	Lys	Ser	Arg	Glu	Ile	Thr
				545					550					555
Thr	Leu	Ala	Asn	Asn	Gln	Cys	Met	Ala	Thr	Glu	Ser	Val	Asp	His
				560					565					570
Glu	Gly	Asn	Phe	Met	Glu	Cys	Gln	Pro	Glu	Ser	Ser	Ile	Ser	His
				575					580					585
Arg	Phe	His	Lys	Asp	Cys	Ala	Ser	Arg	Val	Asn	Asn	Ala	Ser	Tyr
				590					595					600
Cys	Pro	His	Cys	Gly	Glu	Glu	Ser	Ser	Lys	Ala	Lys	Glu	Val	Thr
				605					610					615
Ile	Ala	Lys	Ala	Asp	Thr	Thr	Ser	Thr	Val	Thr	Pro	Val	Pro	Gly
				620					625					630
Gln	Glu	Lys	Gly	Ser	Ala	Leu	Glu	Gly	Arg	Ala	Asp	Thr	Thr	Thr
				635					640					645
Gly	Ser	Ala	Ala	Gly	Pro	Pro	Leu	Ser	Glu	Asp	Asp	Lys	Leu	Gln
				650					655					660
Gly	Ala	Ala	Ser	His	Val	Pro	Glu	Gly	Phe	Asp	Pro	Thr	Gly	Pro
				665					670					675
Ala	Gly	Leu	Gly	Arg	Pro	Thr	Pro	Gly	Leu	Ser	Gln	Gly	Pro	Gly
				680					685					690
Lys	Glu	Thr	Leu	Glu	Ser	Ala	Leu	Ile	Ala	Leu	Asp	Ser	Glu	Lys
				695					700					705
Pro	Lys	Lys	Leu	Arg	Phe	His	Pro	Lys	Gln	Leu	Tyr	Phe	Ser	Ala
				710					715					720
Arg	Gln	Gly	Glu	Leu	Gln	Lys	Val	Leu	Leu	Met	Leu	Val	Asp	Gly
				725					730					735
Ile	Asp	Pro	Asn	Phe	Lys	Met	Glu	His	Gln	Asn	Lys	Arg	Ser	Pro
				740					745					750
Leu	His	Ala	Ala	Ala	Glu	Ala	Gly	His	Val	Asp	Ile	Cys	His	Met
				755					760					765
Leu	Val	Gln	Ala	Gly	Ala	Asn	Ile	Asp	Thr	Cys	Ser	Glu	Asp	Gln
				770					775					780
Arg	Thr	Pro	Leu	Met	Glu	Ala	Ala	Glu	Asn	Asn	His	Leu	Glu	Ala
				785					790					795
Val	Lys	Tyr	Leu	Ile	Lys	Ala	Gly	Ala	Leu	Val	Asp	Pro	Lys	Asp
				800					805					810
Ala	Glu	Gly	Ser	Thr	Cys	Leu	His	Leu	Ala	Ala	Lys	Lys	Gly	His
				815					820					825
Tyr	Glu	Val	Val	Gln	Tyr	Leu	Leu	Ser	Asn	Gly	Gln	Met	Asp	Val
				830					835					840
Asn	Cys	Gln	Asp	Asp	Gly	Glu	Leu	Asp	Thr	His	Asp	Leu	Gly	His
				845					850					855
Arg	Val	Gln	Ala	Arg	Gly	Pro	Arg	Glu	Ala	Ala	Ala	Val	Gln	Gly
				860					865					870
Leu														

&lt;210&gt; 159

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:265552.1.orf2:2002JAN18

&lt;400&gt; 159

```

Thr Ile Ala Tyr Leu Leu Ile Lys Ser Lys Cys Leu Ser Leu Ala
 1          5          10          15
Val Pro Pro Leu Leu Ser Gly Asn Asp Phe Gln Thr Val Glu Glu
          20          25          30
Gly Ser Asn Val Lys Leu Val Cys Asn Val Lys Ala Asn Pro Gln
          35          40          45
Ala Gln Met Met Trp Tyr Lys Asn Ser Ser Leu Leu Asp Leu Glu
          50          55          60
Lys Ser Arg His Gln Ile Gln Gln Thr Ser Glu Ser Phe Gln Leu
          65          70          75
Ser Ile Thr Lys Val Glu Lys Pro Asp Asn Gly Thr Tyr Ser Cys
          80          85          90
Ile Ala Lys Ser Ser Leu Lys Thr Glu Ser Leu Asp Phe His Leu
          95          100          105
Ile Val Lys Asp Lys Thr Val Gly Val Pro Ile Glu Pro Ile Ile
          110          115          120
Ala Ala Cys Val Val Ile Phe Leu Thr Leu Cys Phe Gly Leu Ile
          125          130          135
Ala Arg Arg Lys Lys Ile Met Lys Leu Cys Met Lys Asp Lys Asp
          140          145          150
Pro His Ser Glu Thr Ala Leu
          155

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&lt;210&gt; 160

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:275355.12.orf1:2002JAN18

&lt;400&gt; 160

```

Lys Tyr Glu Phe Asp Asp Tyr Glu Arg Phe Ile Lys Tyr Leu Gly
 1          5          10          15
Gly Leu Asn Phe Met Thr Thr Leu Thr Thr His Lys His Leu Pro
          20          25          30
His Arg Arg Val Ser Pro Asp Leu Leu Ile Leu Pro Cys Thr Phe
          35          40          45
Ala Ser Val Gly Ile Met Trp Ile Asp Ser Val Phe Phe Arg Leu
          50          55          60
Val Asp Ala Leu Lys Leu Gln Asp Gln Leu Lys Ala Pro Val Lys
          65          70          75
Thr Leu Ser Glu Gly Ile Lys Arg Lys Leu Cys Phe Val Leu Ser
          80          85          90
Ile Leu Gly Asn Pro Ser Val Val Leu Leu Asp Glu Pro Ser Thr
          95          100          105
Gly Met Asp Pro Glu Gly Gln Gln Gln Met Trp Gln Val Ile Arg
          110          115          120
Ala Thr Phe Arg Asn Thr Glu Arg Gly Ala Leu Leu Thr Thr His
          125          130          135
Tyr Met Ala Glu Ala Glu Ala Val Cys Asp Arg Val Ala Ile Met
          140          145          150
Val Ser Gly Arg Leu Arg Cys Ile Gly Ser Ile Gln His Leu Lys
          155          160          165
Ser Lys Phe Gly Lys Asp Tyr Leu Leu Glu Met Lys Leu Lys Asn
          170          175          180
Leu Ala Gln Met Glu Pro Leu His Ala Glu Ile Leu Arg Leu Phe

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Pro	Gln	Ala	Ala	185	Gln	Glu	Arg	Phe	190	Ser	Ser	Leu	Met	Val	195	Tyr
				200					205							
Lys	Leu	Pro	Val	215	Glu	Asp	Val	Arg	220	Leu	Ser	Gln	Ala	Phe	225	Phe
				230					235							
Lys	Leu	Glu	Ile	245	Val	Lys	Gln	Ser	250	Asp	Leu	Glu	Glu	Tyr	255	Ser
				260					265							
Leu	Ser	Gln	Ser	275	Thr	Leu	Glu	Gln	280	Phe	Leu	Glu	Leu	Ser	285	Lys
Glu	Gln	Glu	Leu		Gly	Asp	Leu	Glu		Asp	Phe	Asp	Pro	Ser		Val
Lys	Trp	Lys	Leu		Leu	Leu	Gln	Glu		Pro						

<210> 161  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:280014.1.orf1:2002JAN18

Met	Trp	Ile	Val	Asp	Ser	Asn	Ile	Ile	Thr	Ala	Ile	Val	Gln	Leu
1				5					10					15
His	Gly	Leu	Trp	Met	Asp	Cys	Thr	Trp	Tyr	Ser	Thr	Gly	Met	Phe
				20					25					30
Ser	Cys	Ala	Leu	Lys	His	Ser	Ile	Leu	Ser	Leu	Pro	Ile	His	Val
				35					40					45
Gln	Ala	Ala	Arg	Ala	Thr	Met	Val	Leu	Ala	Cys	Val	Leu	Ser	Ala
				50					55					60
Leu	Gly	Ile	Cys	Thr	Ser	Thr	Val	Gly	Met	Lys	Cys	Thr	Arg	Leu
				65					70					75
Gly	Gly	Asp	Arg	Glu	Thr	Lys	Ser	His	Ala	Ser	Phe	Ala	Gly	Gly
				80					85					90
Val	Cys	Phe	Met	Ser	Ala	Gly	Ile	Ser	Ser	Leu	Ile	Ser	Thr	Val
				95					100					105
Trp	Tyr	Thr	Lys	Glu	Ile	Ile	Ala	Asn	Phe	Leu	Asp	Leu	Thr	Val
				110					115					120
Pro	Glu	Ser	Asn	Lys	His	Glu	Pro	Gly	Gly	Ala	Ile	Tyr	Ile	Gly
				125					130					135
Phe	Ile	Ser	Ala	Met	Leu	Leu	Phe	Ile	Ser	Gly	Met	Ile	Phe	
				140					145					

<210> 162  
 <211> 281  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:299937.3.orf3:2002JAN18

Phe	Gly	Gly	Arg	Pro	Ala	Gly	Ala	Ser	Pro	Leu	Leu	Ser	Ser	Lys
1				5					10					15
Leu	Thr	Tyr	Leu	His	Leu	Pro	Ala	Gly	Ile	Lys	Met	Ala	Gly	Tyr
				20					25					30
Ala	Thr	Thr	Pro	Ser	Pro	Met	Gln	Thr	Leu	Gln	Glu	Glu	Ala	Val
				35					40					45
Cys	Ala	Ile	Cys	Leu	Asp	Tyr	Phe	Lys	Asp	Pro	Val	Ser	Ile	Ser
				50					55					60

Cys	Gly	His	Asn	Phe	Cys	Arg	Gly	Cys	Val	Thr	Gln	Leu	Trp	Ser
				65					70					75
Lys	Glu	Asp	Glu	Glu	Asp	Gln	Asn	Glu	Glu	Glu	Asp	Glu	Trp	Glu
				80					85					90
Glu	Glu	Glu	Asp	Glu	Glu	Ala	Val	Gly	Ala	Met	Asp	Gly	Trp	Asp
				95					100					105
Gly	Ser	Ile	Arg	Glu	Val	Leu	Tyr	Arg	Gly	Asn	Ala	Asp	Glu	Glu
				110					115					120
Leu	Phe	Gln	Asp	Gln	Asp	Asp	Asp	Glu	Leu	Trp	Leu	Gly	Asp	Ser
				125					130					135
Gly	Ile	Thr	Asn	Trp	Asp	Asn	Val	Asp	Tyr	Met	Trp	Asp	Glu	Glu
				140					145					150
Glu	Glu	Glu	Glu	Glu	Asp	Gln	Asp	Tyr	Tyr	Leu	Gly	Gly	Leu	Arg
				155					160					165
Pro	Asp	Leu	Arg	Ile	Asp	Val	Tyr	Arg	Glu	Glu	Glu	Ile	Leu	Glu
				170					175					180
Ala	Tyr	Asp	Glu	Asp	Glu	Asp	Glu	Glu	Leu	Tyr	Pro	Asp	Ile	His
				185					190					195
Pro	Pro	Pro	Ser	Leu	Pro	Leu	Pro	Gly	Gln	Phe	Thr	Cys	Pro	Gln
				200					205					210
Cys	Arg	Lys	Ser	Phe	Thr	Arg	Arg	Ser	Phe	Arg	Pro	Asn	Leu	Gln
				215					220					225
Leu	Ala	Asn	Met	Val	Gln	Ile	Ile	Arg	Gln	Met	Cys	Pro	Thr	Pro
				230					235					240
Tyr	Arg	Gly	Asn	Arg	Ser	Asn	Asp	Gln	Gly	Met	Cys	Phe	Lys	His
				245					250					255
Gln	Glu	Ala	Leu	Lys	Leu	Phe	Cys	Glu	Val	Asp	Lys	Glu	Ala	Ile
				260					265					270
Cys	Val	Val	Cys	Arg	Glu	Ser	Arg	Ser	His	Lys				
				275					280					

&lt;210&gt; 163

&lt;211&gt; 703

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:311197.3.orf3:2002JAN18

&lt;400&gt; 163

Gly	Arg	Ser	Ser	Pro	Arg	Ala	Arg	Leu	Arg	Gly	Trp	Thr	Leu	Arg
1				5					10					15
Ala	Pro	Gly	Lys	Glu	Thr	Pro	Ala	Phe	Ala	Thr	Met	Leu	Ser	Ser
				20					25					30
Thr	Asp	Phe	Thr	Phe	Ala	Ser	Trp	Glu	Leu	Val	Val	Arg	Val	Asp
				35					40					45
His	Pro	Asn	Glu	Glu	Gln	Gln	Lys	Asp	Val	Thr	Leu	Arg	Val	Ser
				50					55					60
Gly	Asp	Leu	His	Val	Gly	Gly	Val	Met	Leu	Lys	Leu	Val	Glu	Gln
				65					70					75
Ile	Asn	Ile	Ser	Gln	Asp	Trp	Ser	Asp	Phe	Ala	Leu	Trp	Trp	Glu
				80					85					90
Gln	Lys	His	Cys	Trp	Leu	Leu	Lys	Thr	His	Trp	Thr	Leu	Asp	Lys
				95					100					105
Tyr	Gly	Val	Gln	Ala	Asp	Ala	Lys	Leu	Leu	Phe	Thr	Pro	Gln	His
				110					115					120
Lys	Met	Leu	Arg	Glu	Arg	Leu	Pro	Asn	Leu	Lys	Met	Val	Arg	Leu
				125					130					135
Arg	Val	Ser	Phe	Ser	Ala	Val	Val	Phe	Lys	Ala	Val	Ser	Asp	Ile
				140					145					150
Cys	Lys	Ile	Leu	Asn	Ile	Arg	Arg	Ser	Glu	Glu	Leu	Ser	Leu	Leu
				155					160					165

Lys	Pro	Ser	Gly	Asp	Tyr	Phe	Lys	Lys	Lys	Lys	Lys	Asp	Lys
				170									180
Asn	Asn	Lys	Glu	Pro	Ile	Ile	Glu	Asp	Ile	Leu	Asn	Leu	Ser
				185									195
Ser	Pro	Thr	Ala	Ser	Gly	Ser	Ser	Val	Ser	Pro	Gly	Leu	Tyr
				200									210
Lys	Thr	Met	Thr	Pro	Ile	Tyr	Asp	Pro	Ile	Asn	Gly	Thr	Pro
				215									225
Ser	Ser	Thr	Met	Thr	Trp	Phe	Ser	Asp	Ser	Pro	Leu	Thr	Glu
				230									240
Asn	Cys	Ser	Ile	Leu	Ala	Phe	Ser	Gln	Pro	Pro	Gln	Ser	Pro
				245									255
Ala	Leu	Ala	Asp	Met	Tyr	Gln	Pro	Arg	Ser	Leu	Val	Asp	Lys
				260									270
Lys	Leu	Asn	Ala	Gly	Trp	Leu	Asp	Ser	Ser	Arg	Ser	Leu	Met
				275									285
Gln	Gly	Ile	Gln	Glu	Asp	Glu	Gln	Leu	Leu	Leu	Arg	Phe	Lys
				290									300
Tyr	Ser	Phe	Phe	Asp	Leu	Asn	Pro	Lys	Tyr	Asp	Ala	Val	Arg
				305									315
Asn	Gln	Leu	Tyr	Glu	Gln	Ala	Arg	Trp	Ala	Ile	Leu	Leu	Glu
				320									330
Ile	Asp	Cys	Thr	Glu	Glu	Glu	Met	Leu	Ile	Phe	Ala	Ala	Leu
				335									345
Tyr	His	Ile	Ser	Lys	Leu	Ser	Leu	Ser	Ala	Glu	Thr	Gln	Asp
				350									360
Ala	Gly	Glu	Ser	Glu	Val	Asp	Glu	Ile	Glu	Ala	Ala	Leu	Ser
				365									375
Leu	Glu	Val	Thr	Leu	Glu	Gly	Gly	Lys	Ala	Asp	Ser	Leu	Leu
				380									390
Asp	Ile	Thr	Asp	Ile	Pro	Lys	Leu	Ala	Asp	Asn	Leu	Lys	Leu
				395									405
Arg	Pro	Lys	Lys	Leu	Leu	Pro	Lys	Ala	Phe	Lys	Gln	Tyr	Trp
				410									420
Ile	Phe	Lys	Asp	Thr	Ser	Ile	Ala	Tyr	Phe	Lys	Asn	Lys	Glu
				425									435
Glu	Gln	Gly	Glu	Pro	Leu	Glu	Lys	Leu	Asn	Leu	Arg	Gly	Cys
				440									450
Val	Val	Pro	Asp	Val	Asn	Val	Ala	Gly	Arg	Lys	Phe	Gly	Ile
				455									465
Leu	Leu	Ile	Pro	Val	Ala	Asp	Gly	Met	Asn	Glu	Met	Tyr	Leu
				470									480
Cys	Asp	His	Glu	Asn	Gln	Tyr	Ala	Gln	Trp	Met	Ala	Ala	Cys
				485									495
Leu	Ala	Ser	Lys	Gly	Lys	Thr	Met	Ala	Asp	Ser	Ser	Tyr	Gln
				500									510
Glu	Val	Leu	Asn	Ile	Leu	Ser	Phe	Leu	Arg	Met	Lys	Asn	Arg
				515									525
Ser	Ala	Ser	Gln	Val	Ala	Ser	Ser	Leu	Glu	Asn	Met	Asp	Met
				530									540
Pro	Glu	Cys	Phe	Val	Ser	Pro	Arg	Cys	Ala	Lys	Arg	His	Lys
				545									555
Lys	Gln	Leu	Ala	Ala	Arg	Ile	Leu	Glu	Ala	His	Gln	Asn	Val
				560									570
Gln	Met	Pro	Leu	Val	Glu	Ala	Lys	Leu	Arg	Phe	Ile	Gln	Ala
				575									585
Gln	Ser	Leu	Pro	Glu	Phe	Gly	Leu	Thr	Tyr	Tyr	Leu	Val	Arg
				590									600
Lys	Gly	Ser	Lys	Lys	Asp	Asp	Ile	Leu	Gly	Val	Ser	Tyr	Asn
				605									615
Leu	Ile	Lys	Ile	Asp	Ala	Ala	Thr	Gly	Ile	Pro	Val	Thr	Thr
				620									630
Arg	Phe	Thr	Asn	Ile	Lys	Gln	Trp	Asn	Val	Asn	Trp	Glu	Thr
													Arg

Gln Val Val Ile	635	Glu Phe Asp Gln Asn	640	Val Phe Thr Ala Phe	645
	650		655		660
Cys Leu Ser Ala	665	Asp Cys Lys Ile Val	670	His Glu Tyr Ile Gly	675
	680		685		690
Tyr Ile Phe Leu	695	Ser Thr Arg Ser Lys	700	Asp Gln Asn Glu Thr	
Asp Glu Asp Leu		Phe His Lys Leu Thr		Gly Gly Gln Asp	

&lt;210&gt; 164

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:321069.2.orf1:2002JAN18

&lt;400&gt; 164

Gly Thr His Pro Ser	Thr Val Leu Leu Ser	Pro Leu Ala Gly Val
1	5	10
Glu Leu Pro Val Tyr	Asp Ile Thr Lys Lys	His Leu Ile Leu Ser
20	25	30
Gly Leu Met Gly Asp	Thr Val Tyr Thr His	Phe Leu Ser Ser Phe
35	40	45
Thr Cys Gly Leu Ala	Gly Ala Leu Ala Ser	Asn Pro Val Asp Val
50	55	60
Val Arg Thr Arg Met	Met Asn Gln Arg Val	Leu Arg Asp Gly Arg
65	70	75
Cys Ser Gly Tyr Thr	Gly Thr Leu Asp Cys	Leu Leu Gln Thr Trp
80	85	90
Lys Asn Glu Gly Phe	Phe Ala Leu Tyr Lys	Gly Phe Trp Pro Asn
95	100	105
Trp Leu Arg Leu Gly	Pro Trp Asn Ile Ile	Phe Phe Val Thr Tyr
110	115	120
Glu Gln Leu Lys Lys	Leu Asp Leu	
125		

&lt;210&gt; 165

&lt;211&gt; 1250

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:330900.8.orf2:2002JAN18

&lt;400&gt; 165

Val Asp Glu His Leu	His Glu Asp Asn Gly	Glu Val Glu Val Arg
1	5	10
Arg Ser Cys Arg Ile	Arg Ser Arg Tyr Ser	Gly Val Asn Gln Ser
20	25	30
Met Leu Phe Asp Lys	Leu Ile Thr Asn Thr	Ala Glu Ala Val Leu
35	40	45
Gln Lys Met Asp Asp	Met Lys Lys Met Arg	Arg Gln Arg Met Arg
50	55	60
Glu Leu Glu Asp Leu	Gly Val Phe Asn Glu	Thr Glu Glu Ser Asn
65	70	75
Leu Asn Met Tyr Thr	Arg Gly Lys Gln Lys	Asp Ile Gln Arg Thr
80	85	90
Asp Glu Glu Thr Thr	Asp Asn Gln Glu Gly	Ser Val Glu Ser Ser
95	100	105

Glu	Glu	Gly	Glu	Asp	Gln	Glu	His	Glu	Asp	Asp	Gly	Glu	Asp	Glu
				110					115					120
Asp	Asp	Glu	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp
				125					130					135
Asp	Asp	Glu	Asp	Asp	Glu	Asp	Glu	Glu	Asp	Gly	Glu	Glu	Glu	Asn
				140					145					150
Gln	Lys	Arg	Tyr	Tyr	Leu	Arg	Gln	Arg	Lys	Ala	Thr	Val	Tyr	Tyr
				155					160					165
Gln	Ala	Pro	Leu	Glu	Lys	Pro	Arg	His	Gln	Arg	Lys	Pro	Asn	Ile
				170					175					180
Phe	Tyr	Ser	Gly	Pro	Ala	Ser	Pro	Ala	Arg	Pro	Arg	Tyr	Arg	Leu
				185					190					195
Ser	Ser	Ala	Gly	Pro	Arg	Ser	Pro	Tyr	Cys	Lys	Arg	Met	Asn	Arg
				200					205					210
Arg	Arg	His	Ala	Ile	His	Ser	Ser	Asp	Ser	Thr	Ser	Ser	Ser	Ser
				215					220					225
Ser	Glu	Asp	Glu	Gln	His	Phe	Glu	Arg	Arg	Arg	Lys	Arg	Ser	Arg
				230					235					240
Asn	Arg	Ala	Ile	Asn	Arg	Cys	Leu	Pro	Leu	Asn	Phe	Arg	Lys	Asp
				245					250					255
Glu	Leu	Lys	Gly	Ile	Tyr	Lys	Asp	Arg	Met	Lys	Ile	Gly	Ala	Ser
				260					265					270
Leu	Ala	Asp	Val	Asp	Pro	Met	Gln	Leu	Asp	Ser	Ser	Val	Arg	Phe
				275					280					285
Asp	Ser	Val	Gly	Gly	Leu	Ser	Asn	His	Ile	Ala	Ala	Leu	Lys	Glu
				290					295					300
Met	Val	Val	Phe	Pro	Leu	Leu	Tyr	Pro	Glu	Val	Phe	Glu	Lys	Phe
				305					310					315
Lys	Ile	Gln	Pro	Pro	Arg	Gly	Cys	Leu	Phe	Tyr	Gly	Pro	Pro	Gly
				320					325					330
Thr	Gly	Lys	Thr	Leu	Val	Ala	Arg	Ala	Leu	Ala	Asn	Glu	Cys	Ser
				335					340					345
Gln	Gly	Asp	Lys	Arg	Val	Ala	Phe	Phe	Met	Arg	Lys	Gly	Ala	Asp
				350					355					360
Cys	Leu	Ser	Lys	Trp	Val	Gly	Glu	Ser	Glu	Arg	Gln	Leu	Arg	Leu
				365					370					375
Leu	Phe	Asp	Gln	Ala	Tyr	Gln	Met	Arg	Pro	Ser	Ile	Ile	Phe	Phe
				380					385					390
Asp	Glu	Ile	Asp	Gly	Leu	Ala	Pro	Val	Arg	Ser	Ser	Arg	Gln	Asp
				395					400					405
Gln	Ile	His	Ser	Ser	Ile	Val	Ser	Thr	Leu	Leu	Ala	Leu	Met	Asp
				410					415					420
Gly	Leu	Asp	Ser	Arg	Gly	Glu	Ile	Val	Val	Ile	Gly	Ala	Thr	Asn
				425					430					435
Arg	Leu	Asp	Ser	Ile	Asp	Pro	Ala	Leu	Arg	Arg	Pro	Gly	Arg	Phe
				440					445					450
Asp	Arg	Glu	Phe	Leu	Phe	Ser	Leu	Pro	Asp	Lys	Glu	Ala	Arg	Lys
				455					460					465
Glu	Ile	Leu	Lys	Ile	His	Thr	Arg	Asp	Trp	Asn	Pro	Lys	Pro	Leu
				470					475					480
Asp	Thr	Phe	Leu	Glu	Glu	Leu	Ala	Glu	Asn	Cys	Val	Gly	Tyr	Cys
				485					490					495
Gly	Ala	Asp	Ile	Lys	Ser	Ile	Cys	Ala	Glu	Ala	Ala	Leu	Cys	Ala
				500					505					510
Leu	Arg	Arg	Arg	Tyr	Pro	Gln	Ile	Tyr	Thr	Thr	Ser	Glu	Lys	Leu
				515					520					525
Gln	Leu	Asp	Leu	Ser	Ser	Ile	Asn	Ile	Ser	Ala	Lys	Asp	Phe	Glu
				530					535					540
Val	Ala	Met	Gln	Lys	Met	Ile	Pro	Ala	Ser	Gln	Arg	Ala	Val	Thr
				545					550					555
Ser	Pro	Gly	Gln	Ala	Leu	Ser	Thr	Val	Val	Lys	Pro	Leu	Leu	Gln
				560					565					570
Asn	Thr	Val	Asp	Lys	Ile	Leu	Glu	Ala	Leu	Gln	Arg	Val	Phe	Pro



	575	580	585
His Ala Glu Phe Arg Thr Asn Lys Thr	Leu Asp Ser Asp Ile Ser		
	590	595	600
Cys Pro Leu Leu Glu Ser Asp Leu Ala Tyr Ser Asp Asp Asp Val			
	605	610	615
Pro Ser Val Tyr Glu Asn Gly Leu Ser Gln Lys Ser Ser His Lys			
	620	625	630
Ala Lys Asp Asn Phe Asn Phe Leu His Leu Asn Arg Asn Ala Cys			
	635	640	645
Tyr Gln Pro Met Ser Phe Arg Pro Arg Ile Leu Ile Val Gly Glu			
	650	655	660
Pro Gly Phe Gly Gln Gly Ser His Leu Ala Pro Ala Val Ile His			
	665	670	675
Ala Leu Glu Lys Phe Thr Val Tyr Thr Leu Asp Ile Pro Val Leu			
	680	685	690
Phe Gly Val Ser Thr Thr Ser Pro Glu Glu Thr Cys Ala Gln Val			
	695	700	705
Ile Arg Glu Ala Lys Arg Thr Ala Pro Ser Ile Val Tyr Val Pro			
	710	715	720
His Ile His Val Trp Trp Glu Ile Val Gly Pro Thr Leu Lys Ala			
	725	730	735
Thr Phe Thr Thr Leu Leu Gln Asn Ile Pro Ser Phe Ala Pro Val			
	740	745	750
Leu Leu Leu Ala Thr Ser Asp Lys Pro His Ser Ala Leu Pro Glu			
	755	760	765
Glu Val Gln Glu Leu Phe Ile Arg Asp Tyr Gly Glu Ile Phe Asn			
	770	775	780
Val Gln Leu Pro Asp Lys Glu Glu Arg Thr Lys Phe Phe Glu Asp			
	785	790	795
Leu Ile Leu Lys Gln Ala Ala Lys Pro Pro Ile Ser Lys Lys Lys			
	800	805	810
Ala Val Leu Gln Ala Leu Glu Val Leu Pro Val Ala Pro Pro Pro			
	815	820	825
Glu Pro Arg Ser Leu Thr Ala Glu Glu Val Lys Arg Leu Glu Glu			
	830	835	840
Gln Glu Glu Asp Thr Phe Arg Glu Leu Arg Ile Phe Leu Arg Asn			
	845	850	855
Val Thr His Arg Leu Ala Ile Asp Lys Arg Phe Arg Val Phe Thr			
	860	865	870
Lys Pro Val Asp Pro Asp Glu Val Pro Asp Tyr Val Thr Val Ile			
	875	880	885
Lys Gln Pro Met Asp Leu Ser Ser Val Ile Ser Lys Ile Asp Leu			
	890	895	900
His Lys Tyr Leu Thr Val Lys Asp Tyr Leu Arg Asp Ile Asp Leu			
	905	910	915
Ile Cys Ser Asn Ala Leu Glu Tyr Asn Pro Asp Arg Asp Pro Gly			
	920	925	930
Asp Arg Leu Ile Arg His Arg Ala Cys Ala Leu Arg Asp Thr Ala			
	935	940	945
Tyr Ala Ile Ile Lys Glu Glu Leu Asp Glu Asp Phe Glu Gln Leu			
	950	955	960
Cys Glu Glu Ile Gln Glu Ser Arg Lys Lys Arg Gly Cys Ser Ser			
	965	970	975
Ser Lys Tyr Ala Pro Ser Tyr Tyr His Val Met Pro Lys Gln Asn			
	980	985	990
Ser Thr Leu Val Gly Asp Lys Arg Ser Asp Pro Glu Gln Asn Glu			
	995	1000	1005
Lys Leu Lys Thr Pro Ser Thr Pro Val Ala Cys Ser Thr Pro Ala			
	1010	1015	1020
Gln Leu Lys Arg Lys Ile Arg Lys Lys Ser Asn Trp Tyr Leu Gly			
	1025	1030	1035
Thr Ile Lys Lys Arg Arg Lys Ile Ser Gln Ala Lys Asp Asp Ser			
	1040	1045	1050

Gln Asn Ala Ile Asp His Lys Ile Glu Ser Asp Thr Glu Glu Thr  
 1055 1060 1065  
 Gln Asp Thr Ser Val Asp His Asn Glu Thr Gly Asn Thr Gly Glu  
 1070 1075 1080  
 Ser Ser Val Glu Glu Asn Glu Lys Gln Gln Asn Ala Ser Glu Ser  
 1085 1090 1095  
 Lys Leu Glu Leu Arg Asn Asn Ser Asn Thr Cys Asn Ile Glu Asn  
 1100 1105 1110  
 Glu Leu Glu Asp Ser Arg Lys Thr Thr Ala Cys Thr Glu Leu Arg  
 1115 1120 1125  
 Asp Lys Ile Ala Cys Asn Gly Asp Ala Ser Ser Ser Gln Ile Ile  
 1130 1135 1140  
 His Ile Ser Asp Glu Asn Glu Gly Lys Glu Met Cys Val Leu Arg  
 1145 1150 1155  
 Met Thr Arg Ala Arg Arg Ser Gln Val Glu Gln Gln Gln Leu Ile  
 1160 1165 1170  
 Thr Val Glu Lys Ala Leu Ala Ile Leu Ser Gln Pro Thr Pro Ser  
 1175 1180 1185  
 Leu Val Val Asp His Glu Arg Leu Lys Asn Leu Leu Lys Thr Val  
 1190 1195 1200  
 Val Lys Lys Ser Gln Asn Tyr Asn Ile Phe Gln Leu Glu Asn Leu  
 1205 1210 1215  
 Tyr Ala Val Ile Ser Gln Cys Ile Tyr Arg His Arg Lys Asp His  
 1220 1225 1230  
 Asp Lys Thr Ser Leu Ile Gln Lys Met Glu Gln Glu Val Glu Asn  
 1235 1240 1245  
 Phe Ser Cys Ser Arg  
 1250

<210> 166  
 <211> 705  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:330931.9.orf1:2002JAN18

<400> 166  
 Pro Ile Cys Gly Leu Val Ile Lys Arg Lys Ser Tyr Trp Lys Arg  
 1 5 10 15  
 His Met Val Ile His Thr Gly Leu Lys Ser His Gln Cys Pro Leu  
 20 25 30  
 Cys Pro Phe Arg Cys Ala Arg Lys Asp Asn Leu Lys Ser His Met  
 35 40 45  
 Lys Val His Gln His Gln Asp Arg Gly Glu Thr Phe Gln Cys Gln  
 50 55 60  
 Leu Cys Pro Phe Thr Ser Ser Arg His Phe Ser Leu Lys Leu His  
 65 70 75  
 Met Arg Cys His Gln His Phe Leu Arg Thr Glu Ala Lys Val Lys  
 80 85 90  
 Glu Glu Ile Pro Asp Pro Asp Val Lys Gly Ser Pro His Leu Ser  
 95 100 105  
 Asp Ser Ala Cys Leu Gly Gln Gln Arg Glu Gly Gly Gly Thr Glu  
 110 115 120  
 Leu Val Gly Thr Met Met Thr Ser Asn Thr Pro Glu Arg Thr Ser  
 125 130 135  
 Gln Gly Gly Ala Gly Val Ser Pro Leu Leu Val Lys Glu Glu Pro  
 140 145 150  
 Lys Glu Asp Asn Gly Leu Pro Thr Ser Phe Thr Leu Asn Ala Ala  
 155 160 165  
 Asp Arg Pro Ala Asn His Thr Lys Leu Lys Asp Pro Ser Glu Tyr  
 170 175 180

Val	Ala	Asn	Ser	Ala	Ser	Ala	Leu	Phe	Ser	Gln	Asp	Ile	Ser	Val
				185					190					195
Lys	Met	Ala	Ser	Asp	Phe	Leu	Met	Lys	Leu	Ser	Ala	Ala	Asn	Gln
				200					205					210
Lys	Glu	Pro	Met	Asn	Leu	Asn	Phe	Lys	Val	Lys	Glu	Glu	Pro	Lys
				215					220					225
Glu	Gly	Glu	Ser	Leu	Ser	Thr	Thr	Leu	Pro	Arg	Ser	Ser	Tyr	Val
				230					235					240
Phe	Ser	Pro	Glu	Ser	Glu	Val	Ser	Ala	Pro	Gly	Val	Ser	Glu	Asp
				245					250					255
Ala	Leu	Lys	Pro	Gln	Glu	Gly	Lys	Gly	Ser	Val	Leu	Arg	Arg	Asp
				260					265					270
Val	Ser	Val	Lys	Ala	Ala	Ser	Glu	Leu	Leu	Met	Lys	Leu	Ser	Ala
				275					280					285
Glu	Ser	Tyr	Lys	Glu	Thr	Gln	Met	Val	Lys	Ile	Lys	Glu	Glu	Pro
				290					295					300
Met	Glu	Val	Asp	Ile	Gln	Asp	Ser	His	Val	Ser	Ile	Ser	Pro	Ser
				305					310					315
Arg	Asn	Val	Gly	Tyr	Ser	Thr	Leu	Ile	Gly	Arg	Glu	Lys	Thr	Glu
				320					325					330
Pro	Leu	Gln	Lys	Met	Pro	Glu	Gly	Arg	Val	Pro	Pro	Glu	Arg	Asn
				335					340					345
Leu	Phe	Ser	Gln	Asp	Ile	Ser	Val	Lys	Met	Ala	Ser	Glu	Leu	Leu
				350					355					360
Phe	Gln	Leu	Ser	Glu	Lys	Val	Ser	Lys	Glu	His	Asn	His	Thr	Lys
				365					370					375
Glu	Asn	Thr	Ile	Arg	Thr	Thr	Thr	Ser	Pro	Phe	Phe	Ser	Glu	Asp
				380					385					390
Thr	Phe	Arg	Gln	Ser	Pro	Phe	Thr	Ser	Asn	Ser	Lys	Glu	Leu	Leu
				395					400					405
Pro	Ser	Asp	Ser	Val	Leu	His	Gly	Arg	Ile	Ser	Ala	Pro	Glu	Thr
				410					415					420
Glu	Lys	Ile	Val	Leu	Glu	Ala	Gly	Asn	Gly	Leu	Pro	Ser	Trp	Lys
				425					430					435
Phe	Asn	Asp	Gln	Leu	Phe	Pro	Cys	Asp	Val	Cys	Gly	Lys	Val	Phe
				440					445					450
Gly	Arg	Gln	Gln	Thr	Leu	Ser	Arg	His	Leu	Ser	Leu	His	Thr	Glu
				455					460					465
Glu	Arg	Lys	Tyr	Lys	Cys	His	Leu	Cys	Pro	Tyr	Ala	Ala	Lys	Cys
				470					475					480
Arg	Ala	Asn	Leu	Asn	Gln	His	Leu	Thr	Val	His	Ser	Val	Lys	Leu
				485					490					495
Val	Ser	Thr	Asp	Thr	Glu	Asp	Ile	Val	Ser	Ala	Val	Thr	Ser	Glu
				500					505					510
Gly	Ser	Asp	Gly	Lys	Lys	His	Pro	Tyr	Tyr	Tyr	Ser	Cys	His	Val
				515					520					525
Cys	Gly	Phe	Glu	Thr	Glu	Leu	Asn	Val	Gln	Phe	Val	Ser	His	Met
				530					535					540
Ser	Leu	His	Val	Asp	Lys	Glu	Gln	Trp	Met	Phe	Ser	Ile	Cys	Cys
				545					550					555
Thr	Ala	Cys	Asp	Phe	Val	Thr	Met	Glu	Glu	Ala	Glu	Ile	Lys	Thr
				560					565					570
His	Ile	Gly	Thr	Lys	His	Thr	Gly	Glu	Asp	Arg	Lys	Thr	Pro	Ser
				575					580					585
Glu	Ser	Asn	Ser	Pro	Ser	Ser	Ser	Ser	Leu	Ser	Ala	Leu	Ser	Asp
				590					595					600
Ser	Ala	Asn	Ser	Lys	Asp	Asp	Ser	Asp	Gly	Ser	Gln	Lys	Asn	Lys
				605					610					615
Gly	Gly	Asn	Asn	Leu	Leu	Val	Ile	Ser	Val	Met	Pro	Gly	Ser	Gln
				620					625					630
Pro	Ser	Leu	Asn	Ser	Glu	Glu	Lys	Pro	Glu	Lys	Gly	Phe	Glu	Cys
				635					640					645
Val	Phe	Cys	Asn	Phe	Val	Cys	Lys	Thr	Lys	Asn	Met	Phe	Glu	Arg

His	Leu	Gln	Ile	His	Leu	Ile	Thr	Arg	Met	Phe	Glu	Cys	Asp	Val
				665					670					675
Cys	His	Lys	Phe	Met	Lys	Thr	Pro	Glu	Gln	Leu	Leu	Glu	His	Lys
				680					685					690
Lys	Cys	His	Thr	Val	Pro	Thr	Gly	Gly	Leu	Asn	Ser	Gly	Gln	Trp
				695					700					705

&lt;210&gt; 167

&lt;211&gt; 630

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:330985.1.orf3:2002JAN18

&lt;400&gt; 167

Ser	Pro	Gly	Val	Arg	Val	Arg	Gly	Ala	Gly	Ser	Gly	Ser	Pro	Arg
1				5					10					15
Ala	Ala	Ala	Pro	Pro	Ser	Arg	Arg	His	Ser	Val	Thr	Phe	Val	Pro
				20					25					30
Ser	Gly	Ala	Ala	Arg	Gly	Leu	Ser	Arg	Met	Val	Pro	Ser	Ser	Pro
				35					40					45
Ala	Val	Glu	Lys	Gln	Val	Pro	Val	Glu	Pro	Gly	Pro	Asp	Pro	Glu
				50					55					60
Leu	Arg	Ser	Trp	Arg	Arg	Leu	Val	Cys	Tyr	Leu	Cys	Phe	Tyr	Gly
				65					70					75
Phe	Met	Ala	Gln	Ile	Arg	Pro	Gly	Glu	Ser	Phe	Ile	Thr	Pro	Tyr
				80					85					90
Leu	Leu	Gly	Pro	Asp	Lys	Asn	Phe	Thr	Arg	Glu	Gln	Val	Thr	Asn
				95					100					105
Glu	Ile	Thr	Pro	Val	Leu	Ser	Tyr	Ser	Tyr	Leu	Ala	Val	Leu	Val
				110					115					120
Pro	Val	Phe	Leu	Leu	Thr	Asp	Tyr	Leu	Arg	Tyr	Thr	Pro	Val	Leu
				125					130					135
Leu	Leu	Gln	Gly	Leu	Ser	Phe	Val	Ser	Val	Trp	Leu	Leu	Leu	Leu
				140					145					150
Leu	Gly	His	Ser	Val	Ala	His	Met	Gln	Leu	Met	Glu	Leu	Phe	Tyr
				155					160					165
Ser	Val	Thr	Met	Ala	Ala	Arg	Ile	Ala	Tyr	Ser	Ser	Tyr	Ile	Phe
				170					175					180
Ser	Leu	Val	Arg	Pro	Ala	Arg	Tyr	Gln	Arg	Val	Ala	Gly	Tyr	Ser
				185					190					195
Arg	Ala	Ala	Val	Leu	Leu	Gly	Val	Phe	Thr	Ser	Ser	Val	Leu	Gly
				200					205					210
Gln	Leu	Leu	Val	Thr	Val	Gly	Arg	Val	Ser	Phe	Ser	Thr	Leu	Asn
				215					220					225
Tyr	Ile	Ser	Leu	Ala	Phe	Leu	Thr	Phe	Ser	Val	Val	Leu	Ala	Leu
				230					235					240
Phe	Leu	Lys	Arg	Pro	Lys	Arg	Ser	Leu	Phe	Phe	Asn	Arg	Asp	Asp
				245					250					255
Arg	Gly	Arg	Cys	Glu	Thr	Ser	Ala	Ser	Glu	Leu	Glu	Arg	Met	Asn
				260					265					270
Pro	Gly	Pro	Gly	Gly	Lys	Leu	Gly	His	Ala	Leu	Arg	Val	Ala	Cys
				275					280					285
Gly	Asp	Ser	Val	Leu	Ala	Arg	Met	Leu	Arg	Glu	Leu	Gly	Asp	Ser
				290					295					300
Leu	Arg	Arg	Pro	Gln	Leu	Arg	Leu	Trp	Ser	Leu	Trp	Trp	Val	Phe
				305					310					315
Asn	Ser	Ala	Gly	Tyr	Tyr	Leu	Val	Val	Tyr	Tyr	Val	His	Ile	Leu
				320					325					330

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Trp Asn Glu Val Asp Pro Thr Thr Asn Ser Ala Arg Val Tyr Asn
335 340 345
Gly Ala Ala Asp Ala Ala Ser Thr Leu Leu Gly Ala Ile Thr Ser
350 355 360
Phe Ala Ala Gly Phe Val Lys Ile Arg Trp Ala Arg Trp Ser Lys
365 370 375
Leu Leu Ile Ala Gly Val Thr Ala Thr Gln Ala Gly Leu Val Phe
380 385 390
Leu Leu Ala His Thr Arg His Pro Ser Ser Ile Trp Leu Cys Tyr
395 400 405
Ala Ala Phe Val Leu Phe Arg Gly Ser Tyr Gln Phe Leu Val Pro
410 415 420
Ile Ala Thr Phe Gln Ile Ala Ser Ser Leu Ser Lys Glu Leu Cys
425 430 435
Ala Leu Val Phe Gly Val Asn Thr Phe Phe Ala Thr Ile Val Lys
440 445 450
Thr Ile Ile Thr Phe Ile Val Ser Asp Val Arg Gly Leu Gly Leu
455 460 465
Pro Val Arg Lys Gln Phe Gln Leu Tyr Ser Val Tyr Phe Leu Ile
470 475 480
Leu Ser Ile Ile Tyr Phe Leu Gly Ala Met Leu Asp Gly Leu Arg
485 490 495
His Cys Gln Arg Gly His His Pro Arg Gln Pro Pro Ala Gln Gly
500 505 510
Leu Arg Ser Ala Ala Glu Glu Lys Ala Ala Gln Ala Leu Ser Val
515 520 525
Gln Asp Lys Gly Leu Gly Gly Leu Gln Pro Ala Gln Ser Pro Pro
530 535 540
Leu Ser Pro Glu Asp Ser Leu Gly Ala Val Gly Pro Ala Ser Leu
545 550 555
Glu Gln Arg Gln Ser Asp Pro Tyr Leu Ala Gln Ala Pro Ala Pro
560 565 570
Gln Ala Ala Glu Phe Leu Ser Pro Val Thr Thr Pro Ser Pro Cys
575 580 585
Thr Leu Cys Ser Ala Gln Ala Ser Gly Pro Glu Ala Ala Asp Glu
590 595 600
Thr Cys Pro Gln Leu Ala Val His Pro Pro Gly Val Ser Lys Leu
605 610 615
Gly Leu Gln Cys Leu Pro Ser Asp Gly Val Gln Asn Val Asn Gln
620 625 630

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&lt;210&gt; 168

&lt;211&gt; 389

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:332027.9.orf3:2002JAN18

&lt;400&gt; 168

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Arg Met Pro Phe Met Trp Leu Glu Ser Gly Ile Pro Asn Leu Gly
1 5 10 15
Val Trp Pro Asn Arg Ile His Thr Thr Ala Glu Lys Tyr Arg Glu
20 25 30
Tyr Glu Ala Arg Glu Gln Thr Asp Gln Thr Gln Ala Gln Glu Leu
35 40 45
His Arg Ser Gln Asp Arg Asp Phe Glu Thr Met Ala Lys Leu His
50 55 60
Ile Pro Val Met Val Asp Glu Val Val His Cys Leu Ser Pro Gln
65 70 75
Lys Gly Gln Ile Phe Leu Asp Met Thr Phe Gly Ser Gly Gly His

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Thr	Lys	Ala	Ile	Leu	Gln	Lys	Glu	Ser	Asp	Ile	Val	Leu	Tyr	Ala
				95					100					105
Leu	Asp	Arg	Asp	Pro	Thr	Ala	Tyr	Ala	Leu	Ala	Glu	His	Leu	Ser
				110					115					120
Glu	Leu	Tyr	Pro	Lys	Gln	Ile	Arg	Ala	Met	Leu	Gly	Gln	Phe	Ser
				125					130					135
Gln	Ala	Glu	Ala	Leu	Leu	Met	Lys	Ala	Gly	Val	Gln	Pro	Gly	Thr
				140					145					150
Phe	Asp	Gly	Val	Leu	Met	Asp	Leu	Gly	Cys	Ser	Ser	Met	Gln	Leu
				155					160					165
Asp	Thr	Pro	Glu	Arg	Gly	Phe	Ser	Leu	Arg	Lys	Asp	Gly	Pro	Leu
				170					175					180
Asp	Met	Arg	Met	Asp	Gly	Gly	Arg	Tyr	Pro	Asp	Met	Pro	Thr	Ala
				185					190					195
Ala	Asp	Val	Val	Asn	Ala	Leu	Asp	Gln	Gln	Ala	Leu	Ala	Ser	Ile
				200					205					210
Leu	Arg	Thr	Tyr	Gly	Glu	Glu	Lys	His	Ala	Lys	Lys	Ile	Ala	Ser
				215					220					225
Ala	Ile	Val	Gln	Ala	Arg	Ser	Ile	Tyr	Pro	Ile	Thr	Arg	Thr	Gln
				230					235					240
Gln	Leu	Ala	Ser	Ile	Val	Ala	Gly	Ala	Phe	Pro	Pro	Ser	Ala	Ile
				245					250					255
Tyr	Thr	Arg	Lys	Asp	Leu	Leu	Gln	Arg	Ser	Thr	His	Ile	Ala	Thr
				260					265					270
Lys	Thr	Phe	Gln	Ala	Leu	Arg	Ile	Phe	Val	Asn	Asn	Glu	Leu	Asn
				275					280					285
Glu	Leu	Tyr	Thr	Gly	Leu	Lys	Thr	Ala	Gln	Lys	Phe	Leu	Arg	Pro
				290					295					300
Gly	Gly	Arg	Leu	Val	Ala	Leu	Ser	Phe	His	Ser	Leu	Glu	Asp	Arg
				305					310					315
Ile	Val	Lys	Arg	Phe	Leu	Leu	Gly	Ile	Ser	Met	Thr	Glu	Arg	Phe
				320					325					330
Asn	Leu	Ser	Val	Arg	Gln	Gln	Val	Met	Lys	Thr	Ser	Gln	Leu	Gly
				335					340					345
Ser	Asp	His	Glu	Asn	Thr	Glu	Glu	Val	Ser	Met	Arg	Arg	Ala	Pro
				350					355					360
Leu	Met	Trp	Glu	Leu	Ile	His	Lys	Lys	Val	Leu	Ser	Pro	Gln	Asp
				365					370					375
Gln	Asp	Val	Gln	Asp	Asn	Pro	Gln	Arg	Ala	Leu	Ser	Gln	Ala	
				380					385					

&lt;210&gt; 169

&lt;211&gt; 381

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:335377.8.orf2:2002JAN18

&lt;400&gt; 169

Arg	Glu	Ala	Val	Gln	Asp	Gly	Cys	Thr	Leu	Pro	Ala	Pro	Arg	Ser
1				5					10					15
Ser	Gly	Cys	Ser	Leu	Gln	Leu	Ser	Pro	Glu	Ser	Leu	Lys	Arg	Glu
				20					25					30
Pro	Ala	Ser	Cys	Leu	Pro	Gly	Ala	Met	Glu	Ala	Val	Glu	Leu	Ala
				35					40					45
Arg	Lys	Leu	Gln	Glu	Glu	Ala	Thr	Cys	Ser	Ile	Cys	Leu	Asp	Tyr
				50					55					60
Phe	Thr	Asp	Pro	Val	Met	Thr	Thr	Cys	Gly	His	Asn	Phe	Cys	Arg
				65					70					75
Ala	Cys	Ile	Gln	Leu	Ser	Trp	Glu	Lys	Ala	Arg	Gly	Lys	Lys	Gly

				80					85					90
Arg	Arg	Lys	Arg	Lys	Gly	Ser	Phe	Pro	Cys	Pro	Glu	Cys	Arg	Glu
				95					100					105
Met	Ser	Pro	Gln	Arg	Asn	Leu	Leu	Pro	Asn	Arg	Leu	Leu	Thr	Lys
				110					115					120
Val	Ala	Glu	Met	Ala	Gln	Gln	His	Pro	Gly	Leu	Gln	Lys	Gln	Asp
				125					130					135
Leu	Cys	Gln	Glu	His	His	Glu	Pro	Leu	Lys	Leu	Phe	Cys	Gln	Lys
				140					145					150
Asp	Gln	Ser	Pro	Ile	Cys	Val	Val	Cys	Arg	Glu	Ser	Arg	Glu	His
				155					160					165
Arg	Leu	His	Arg	Val	Leu	Pro	Ala	Glu	Glu	Ala	Val	Gln	Gly	Tyr
				170					175					180
Lys	Leu	Lys	Leu	Glu	Glu	Asp	Met	Glu	Tyr	Leu	Arg	Glu	Gln	Ile
				185					190					195
Thr	Arg	Thr	Gly	Asn	Leu	Gln	Ala	Arg	Glu	Glu	Gln	Ser	Leu	Ala
				200					205					210
Glu	Trp	Gln	Gly	Lys	Val	Asn	Gly	Ala	Glu	Arg	Thr	His	Cys	Ala
				215					220					225
Gly	Val	Glu	Lys	Met	Asn	Leu	Tyr	Leu	Val	Glu	Glu	Glu	Gln	Arg
				230					235					240
Leu	Leu	Gln	Ala	Leu	Glu	Thr	Glu	Glu	Glu	Glu	Thr	Ala	Ser	Arg
				245					250					255
Leu	Arg	Glu	Ser	Val	Ala	Cys	Leu	Asp	Arg	Gln	Gly	His	Ser	Leu
				260					265					270
Glu	Leu	Leu	Leu	Leu	Gln	Leu	Glu	Glu	Arg	Ser	Thr	Gln	Gly	Pro
				275					280					285
Leu	Gln	Met	Leu	Gln	Asp	Met	Lys	Glu	Pro	Leu	Ser	Arg	Lys	Asn
				290					295					300
Asn	Val	Ser	Val	Gln	Cys	Pro	Glu	Val	Ala	Pro	Pro	Thr	Arg	Pro
				305					310					315
Arg	Thr	Val	Cys	Arg	Val	Pro	Gly	Gln	Ile	Glu	Val	Leu	Arg	Gly
				320					325					330
Phe	Leu	Gly	Lys	Trp	Ala	Pro	Arg	Ala	Arg	Thr	Ser	Asp	Pro	Gly
				335					340					345
Ser	Leu	Gly	Asp	Ala	Pro	Leu	Tyr	Pro	Leu	Ala	Ser	Glu	Ala	Thr
				350					355					360
Asn	Gly	Gly	Gly	Ser	Thr	Ser	Ala	Leu	Pro	Gly	Asp	Gly	His	Trp
				365					370					375
Leu	Phe	Thr	Val	Pro	Ser									
				380										

&lt;210&gt; 170

&lt;211&gt; 659

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:337452.25.orf3:2002JAN18

&lt;400&gt; 170

Ile	Ser	Ile	His	Pro	Leu	Cys	Phe	Ala	Leu	Glu	Leu	Ala	Pro	Leu
1				5					10					15
Ser	Ser	Leu	Asn	Thr	Val	Leu	Ser	Glu	Asn	Ala	Arg	Asp	Ser	Ser
				20					25					30
Phe	Ile	Pro	Leu	Gly	His	Met	Leu	Thr	Gln	Lys	Ile	Ala	Tyr	Gln
				35					40					45
Ile	Ala	Ser	Gly	Leu	Ala	Tyr	Leu	His	Lys	Lys	Asn	Ile	Ile	Phe
				50					55					60
Cys	Asp	Leu	Lys	Ser	Asp	Asn	Ile	Leu	Val	Trp	Ser	Leu	Asp	Val
				65					70					75
Lys	Glu	His	Ile	Asn	Ile	Lys	Leu	Ser	Asp	Tyr	Gly	Ile	Ser	Arg

Gln Ser Phe His	80	Gly Ala Leu Gly	85	Val Glu Gly Thr Pro	90
	95		100		105
Tyr Gln Ala Pro	110	Glu Ile Arg Pro Arg	115	Ile Val Tyr Asp Glu	120
Val Asp Met Phe	125	Ser Tyr Gly Met Val	130	Leu Tyr Glu Leu Leu	135
Gly Gln Arg Pro	140	Ala Leu Gly His His	145	Gln Leu Gln Ile Ala	150
Lys Leu Ser Lys	155	Gly Ile Arg Pro Val	160	Leu Gly Gln Pro Glu	165
Val Gln Phe Arg	170	Arg Leu Gln Ala Leu	175	Met Met Glu Cys Trp	180
Thr Lys Pro Glu	185	Lys Arg Pro Leu Ala	190	Leu Ser Val Val Ser	195
Met Lys Asp Pro	200	Thr Phe Ala Thr Phe	205	Met Tyr Glu Leu Cys	210
Gly Lys Gln Thr	215	Ala Phe Phe Ser Ser	220	Gln Gly Gln Glu Tyr	225
Val Val Phe Trp	230	Asp Gly Lys Glu Glu	235	Ser Arg Asn Tyr Thr	240
Val Asn Thr Glu	245	Lys Gly Leu Met Glu	250	Val Gln Arg Met Cys	255
Pro Gly Met Lys	260	Val Ser Cys Gln Leu	265	Gln Val Gln Arg Ser	270
Trp Thr Ala Thr	275	Glu Asp Gln Lys Ile	280	Tyr Ile Tyr Thr Leu	285
Gly Met Cys Pro	290	Leu Asn Thr Pro Gln	295	Gln Ala Leu Asp Thr	300
Ala Val Val Thr	305	Cys Phe Leu Ala Val	310	Pro Val Ile Lys Lys	315
Ser Tyr Leu Val	320	Leu Ala Gly Leu Ala	325	Asp Gly Leu Val Ala	330
Phe Pro Val Val	335	Arg Gly Thr Pro Lys	340	Asp Ser Cys Ser Tyr	345
Cys Ser His Thr	350	Ala Asn Arg Ser Lys	355	Phe Ser Ile Ala Asp	360
Asp Ala Arg Gln	365	Asn Pro Tyr Pro Val	370	Lys Ala Met Glu Val	375
Asn Ser Gly Ser	380	Glu Val Trp Tyr Ser	385	Asn Gly Pro Gly Leu	390
Val Ile Asp Cys	395	Ala Ser Leu Glu Ile	400	Cys Arg Arg Leu Glu	405
Tyr Met Ala Pro	410	Ser Met Val Thr Ser	415	Val Val Cys Ser Ser	420
Gly Arg Gly Glu	425	Glu Val Val Trp Cys	430	Leu Asp Asp Lys Ala	435
Ser Leu Val Met	440	Tyr His Ser Thr Thr	445	Tyr Gln Leu Cys Ala	450
Tyr Phe Cys Gly	455	Val Pro Ser Pro Leu	460	Arg Asp Met Phe Pro	465
Arg Pro Leu Asp	470	Thr Glu Pro Pro Ala	475	Ala Ser His Thr Ala	480
Pro Lys Val Pro	485	Glu Gly Asp Ser Ile	490	Ala Asp Val Ser Ile	495
Tyr Ser Glu Glu	500	Leu Gly Thr Gln Ile	505	Leu Ile His Gln Glu	510
Leu Thr Asp Tyr	515	Cys Ser Met Ser Ser	520	Tyr Ser Ser Ser Pro	525
Arg Gln Ala Ala	530	Arg Ser Pro Ser Ser	535	Leu Pro Ser Ser Pro	540
Ser Ser Ser Ser	545	Val Pro Phe Ser Thr	550	Asp Cys Glu Asp Ser	555



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Met Leu His Met Pro Gly Ala Ala Ser Asp Arg Ser Glu His Asp
                    560                    565                    570
Leu Thr Pro Met Asp Gly Glu Thr Phe Ser Gln His Leu Gln Ala
                    575                    580                    585
Val Lys Ile Leu Ala Val Arg Asp Leu Ile Trp Val Pro Arg Arg
                    590                    595                    600
Gly Gly Asp Val Ile Val Ile Gly Leu Glu Lys Asp Ser Glu Ala
                    605                    610                    615
Gln Arg Gly Arg Val Ile Ala Val Leu Lys Ala Arg Glu Leu Thr
                    620                    625                    630
Pro His Gly Ile Met Pro Val Ser Ser Val Lys Val Cys Trp Ala
                    635                    640                    645
Gly Trp Pro Val Arg Asp Met Val Tyr Met Ala Ala Val Met
                    650                    655

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&lt;210&gt; 171

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:340580.16.orf2:2002JAN18

&lt;400&gt; 171

```

Ile Lys His Ser Met Phe Phe Ser Phe Ser Leu Leu Leu Leu Leu
 1          5          10          15
Ser Phe Gly Ile Phe Asn Leu Lys Cys Phe Pro Leu Val Val Gly
          20          25          30
Phe Ile Leu Pro Leu Pro Leu Pro Phe Ser Tyr Tyr Ser Glu Tyr
          35          40          45
Lys Pro Ala Lys Leu Ser Gln Ile Arg Gln Ile Tyr His Thr Glu
          50          55          60
Leu Glu Lys Tyr Glu Gln Ala Cys Asn Glu Phe Thr Thr Leu Val
          65          70          75
Met Asn Leu Leu Arg Glu Gln Ser Arg Thr Arg Pro Ile Ser Pro
          80          85          90
Lys Glu Ile Glu Arg Met Val Ser Ile Ile His Arg Lys Phe Ser
          95          100         105
Ser Ile Gln Met Gln Leu Lys Gln Ser Thr Cys Glu Ala Val Met
          110         115         120
Ile Leu Arg Ser Arg Phe Leu Asp Ala Arg Arg Lys Arg Arg Asn
          125         130         135
Phe Asn Lys Gln Ala Thr Glu Ile Leu Asn Glu Tyr Phe Tyr Ser
          140         145         150
His Leu Ser Asn Pro Tyr Pro Ser Glu Glu Ala Lys Glu Glu Leu
          155         160         165
Ala Lys Lys Cys Gly Ile Thr Val Ser Gln Val Ser Asn Trp Phe
          170         175         180
Gly Asn Lys Arg Ile Arg Tyr Lys Lys Asn Ile Gly Lys Phe Gln
          185         190         195
Glu Glu Ala Asn Ile Tyr Cys Cys Gln Asn Ser Cys His Cys Tyr
          200         205         210
Gln Cys Val Ser Pro Trp Lys Pro Ser
          215

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&lt;210&gt; 172

&lt;211&gt; 438

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:350272.6.orf2:2002JAN18

&lt;400&gt; 172

Arg	Pro	Arg	Ala	Val	Gly	His	Gly	Gly	Pro	Gly	Pro	Gly	Leu	Arg
1				5					10					15
Arg	Ser	Arg	Val	Ala	Gly	Arg	Gly	Arg	Pro	Arg	Leu	His	His	Leu
			20						25					30
Pro	Gly	Leu	Leu	Asp	Trp	Pro	Ala	Thr	Leu	Pro	Cys	Gly	His	Ser
			35						40					45
Phe	Cys	Arg	His	Cys	Leu	Glu	Ala	Leu	Trp	Gly	Ala	Arg	Asp	Ala
			50						55					60
Arg	Arg	Trp	Ala	Cys	Pro	Thr	Cys	Arg	Gln	Gly	Ala	Ala	Gln	Gln
			65						70					75
Pro	His	Leu	Arg	Lys	Asn	Thr	Leu	Leu	Gln	Asp	Leu	Ala	Asp	Lys
			80						85					90
Tyr	Arg	Arg	Ala	Ala	Arg	Glu	Ile	Gln	Ala	Gly	Ser	Asp	Pro	Ala
			95						100					105
His	Cys	Pro	Cys	Pro	Gly	Ser	Ser	Ser	Leu	Ser	Ser	Ala	Ala	Ala
			110						115					120
Arg	Pro	Arg	Arg	Arg	Pro	Glu	Leu	Gln	Arg	Val	Ala	Val	Glu	Lys
			125						130					135
Ser	Ile	Thr	Glu	Val	Ala	Gln	Glu	Leu	Thr	Glu	Leu	Val	Glu	His
			140						145					150
Leu	Val	Asp	Ile	Val	Arg	Ser	Leu	Gln	Asn	Gln	Arg	Pro	Leu	Ser
			155						160					165
Glu	Ser	Gly	Pro	Asp	Asn	Glu	Leu	Ser	Ile	Leu	Gly	Lys	Ala	Phe
			170						175					180
Ser	Ser	Gly	Val	Asp	Leu	Ser	Met	Ala	Ser	Pro	Lys	Leu	Val	Thr
			185						190					195
Ser	Asp	Thr	Ala	Ala	Gly	Lys	Ile	Arg	Asp	Ile	Leu	His	Asp	Leu
			200						205					210
Glu	Glu	Ile	Gln	Glu	Lys	Leu	Gln	Glu	Ser	Val	Thr	Trp	Lys	Glu
			215						220					225
Ala	Pro	Glu	Ala	Gln	Met	Gln	Gly	Glu	Leu	Leu	Glu	Ala	Pro	Ser
			230						235					240
Ser	Ser	Ser	Cys	Pro	Leu	Pro	Asp	Gln	Ser	His	Pro	Ala	Leu	Arg
			245						250					255
Arg	Ala	Ser	Arg	Phe	Ala	Gln	Trp	Ala	Ile	His	Pro	Thr	Phe	Asn
			260						265					270
Leu	Lys	Ser	Leu	Ser	Cys	Ser	Leu	Glu	Val	Ser	Lys	Asp	Ser	Arg
			275						280					285
Thr	Val	Thr	Val	Ser	His	Arg	Pro	Gln	Pro	Tyr	Arg	Trp	Ser	Cys
			290						295					300
Glu	Arg	Phe	Ser	Thr	Ser	Gln	Val	Leu	Cys	Ser	Gln	Ala	Leu	Ser
			305						310					315
Ser	Gly	Lys	His	Tyr	Trp	Glu	Val	Asp	Thr	Arg	Asn	Cys	Ser	His
			320						325					330
Trp	Ala	Val	Gly	Val	Ala	Ser	Trp	Glu	Met	Ser	Arg	Asp	Gln	Val
			335						340					345
Leu	Gly	Arg	Thr	Met	Asp	Ser	Cys	Cys	Val	Glu	Trp	Lys	Gly	Thr
			350						355					360
Ser	Gln	Leu	Ser	Ala	Trp	His	Met	Val	Lys	Glu	Thr	Val	Leu	Gly
			365						370					375
Ser	Asp	Arg	Pro	Gly	Val	Val	Gly	Ile	Trp	Leu	Asn	Leu	Glu	Glu
			380						385					390
Gly	Lys	Leu	Ala	Phe	Tyr	Ser	Val	Asp	Asn	Gln	Glu	Lys	Leu	Leu
			395						400					405
Tyr	Glu	Cys	Thr	Ile	Ser	Ala	Ser	Ser	Pro	Leu	Tyr	Pro	Ala	Phe
			410						415					420
Trp	Leu	Tyr	Gly	Leu	His	Pro	Gly	Asn	Tyr	Leu	Ile	Ile	Lys	Gln
			425						430					435
Val	Lys	Val												

<210> 173  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:397228.1.orf1:2002JAN18

<400> 173  
 Arg Arg Arg Arg Ala Met Ala Ala Gln Leu Leu Glu Glu Lys Leu  
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 Thr Cys Ala Ile Cys Leu Gly Leu Tyr Gln Asp Pro Val Thr Leu  
                   20                  25                  30  
 Pro Cys Gly His Asn Phe Cys Gly Ala Cys Ile Arg Asp Trp Trp  
                   35                  40                  45  
 Asp Arg Cys Gly Lys Ala Cys Pro Glu Cys Arg Glu Pro Phe Pro  
                   50                  55                  60  
 Asp Gly Ala Glu Leu Arg Arg Asn Val Ala Leu Ser Gly Val Leu  
                   65                  70                  75  
 Glu Val Val Arg Ala Gly Pro Ala Arg Asp Pro Gly Pro Asp Pro  
                   80                  85                  90  
 Gly Pro Gly Pro Asp Pro Ala Ala Arg Cys Pro Arg His Gly Arg  
                   95                  100                 105  
 Pro

<210> 174  
 <211> 357  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:401325.41.orf2:2002JAN18

<400> 174  
 Arg Trp Pro Pro Pro Asp Ala Gly Leu Cys Gly Ser Gly Pro Leu  
   1                  5                  10                  15  
 Ser Ser Pro Ser Cys Cys Arg Tyr Arg Arg Cys Cys Arg Arg Leu  
                   20                  25                  30  
 Arg Pro Pro Leu Arg Ser Val Val Gln Pro Gly Pro Arg Thr Met  
                   35                  40                  45  
 Ser Leu Ser Arg Ser Glu Glu Met His Arg Leu Thr Glu Asn Val  
                   50                  55                  60  
 Tyr Lys Thr Ile Met Glu Gln Phe Asn Pro Ser Leu Arg Asn Phe  
                   65                  70                  75  
 Ile Ala Met Gly Lys Asn Tyr Glu Lys Ala Leu Ala Gly Val Thr  
                   80                  85                  90  
 Tyr Ala Ala Lys Gly Tyr Phe Asp Ala Leu Val Lys Met Gly Glu  
                   95                  100                 105  
 Leu Ala Ser Glu Ser Gln Gly Ser Lys Glu Leu Gly Asp Val Leu  
                   110                 115                 120  
 Phe Gln Met Ala Glu Val His Arg Gln Ile Gln Asn Gln Leu Glu  
                   125                 130                 135  
 Glu Met Leu Lys Ser Phe His Asn Glu Leu Leu Thr Gln Leu Glu  
                   140                 145                 150  
 Gln Lys Val Glu Leu Asp Ser Arg Tyr Leu Ser Ala Ala Leu Lys  
                   155                 160                 165  
 Lys Tyr Gln Thr Glu Gln Arg Ser Lys Gly Asp Ala Leu Asp Lys  
                   170                 175                 180  
 Cys Gln Ala Glu Leu Lys Lys Leu Arg Lys Lys Ser Gln Gly Ser  
                   185                 190                 195

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Lys Asn Pro Gln Lys Tyr Ser Asp Lys Glu Leu Gln Tyr Ile Asp
200 205 210
Ala Ile Ser Asn Lys Gln Gly Glu Leu Glu Asn Tyr Val Ser Asp
215 220 225
Gly Tyr Lys Thr Ala Leu Thr Glu Glu Arg Arg Arg Phe Cys Phe
230 235 240
Leu Val Glu Lys Gln Cys Ala Val Ala Lys Asn Ser Ala Ala Tyr
245 250 255
His Ser Lys Gly Lys Glu Leu Leu Ala Gln Lys Leu Pro Leu Trp
260 265 270
Gln Gln Ala Cys Ala Asp Pro Ser Lys Ile Pro Glu Arg Ala Val
275 280 285
Gln Leu Met Gln Gln Val Ala Ser Asn Gly Ala Thr Leu Pro Ser
290 295 300
Ala Cys Arg Pro Pro Ser Gln Pro Gly His Phe Arg Pro His Ser
305 310 315
Gly Gly Gln Ala Pro Ala Gly Ala Pro Arg Ala Gly Thr Val Arg
320 325 330
Gly Ala Asp Val Cys Pro Gly Glu His Thr His His Glu Arg Arg
335 340 345
His Arg Pro Gly Trp Arg Gly Leu Gln Pro Val Gly
350 355

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&lt;210&gt; 175

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:402029.14.orf3:2002JAN18

&lt;400&gt; 175

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Met Ala Leu Phe Ser Cys Arg Asn Ala Val Glu Glu Gly Lys Gly
1 5 10 15
Ile Phe Tyr Asn Ile Lys Asn Phe Val Arg Phe Gln Leu Ser Thr
20 25 30
Ser Ile Ser Ala Leu Ser Leu Ile Thr Leu Ser Thr Val Phe Asn
35 40 45
Leu Pro Ser Pro Leu Asn Ala Met Gln Ile Leu Trp Ile Asn Ile
50 55 60
Ile Met Asp Gly Pro Pro Ala Gln Arg Ser Ser Gln Lys Thr Glu
65 70 75
Val Cys Cys Thr Gly Val Arg Leu Gly Val Glu Gly Arg Gly Glu
80 85 90
Ser Thr Trp Ala Gly Arg Ala Gly Leu Gly Val Glu Pro Val Asp
95 100 105
Lys Asp Ala Phe Arg Gln Pro Pro Arg Ser Val Arg Asp Thr Ile
110 115 120
Leu Ser Arg Ala Leu Ile Leu Lys Ile Leu Met Ser Ala Ala Ile
125 130 135
Ile Ile Ser Gly Thr Leu Phe Ile Phe Trp Lys Glu Met Pro Glu
140 145 150
Asp Arg Ala Ser Thr Pro Arg Thr Thr Thr Met Thr Phe Thr Cys
155 160 165
Phe Val Phe Phe Asp Leu Phe Asn Ala Leu Thr Cys Arg Ser Gln
170 175 180
Thr Lys Leu Ile Phe Glu Ile Gly Phe Leu Arg Asn His Met Phe
185 190 195
Leu Tyr Ser Val Leu Gly Ser Ile Leu Gly Gln Leu Ala Val Ile
200 205 210
Tyr Ile Pro Pro Leu Gln Arg Val Phe Gln Thr Glu Asn Leu Gly
215 220 225

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Ala	Leu	Asp	Leu	Leu	Phe	Leu	Thr	Gly	Leu	Ala	Ser	Ser	Val	Phe
				230					235					240
Ile	Leu	Ser	Glu	Leu	Leu	Lys	Leu	Cys	Glu	Lys	Tyr	Cys	Cys	Ser
				245					250					255
Pro	Lys	Arg	Val	Gln	Met	His	Pro	Glu	Asp	Val				
				260					265					

&lt;210&gt; 176

&lt;211&gt; 470

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:407233.2.orf3:2002JAN18

&lt;400&gt; 176

Pro	Arg	Cys	Pro	Cys	His	Gln	Asp	Leu	His	Met	Pro	Ser	Cys	Val
1				5					10					15
Pro	Pro	Gly	Val	Pro	Val	Ser	Asn	Val	Asn	Leu	Glu	Ile	Arg	Pro
				20					25					30
Thr	Gly	Gly	Gln	Leu	Ile	Glu	Gly	Glu	Asn	Met	Val	Leu	Ile	Cys
				35					40					45
Ser	Val	Ala	Gln	Gly	Ser	Gly	Thr	Val	Thr	Phe	Ser	Trp	His	Lys
				50					55					60
Glu	Gly	Arg	Val	Arg	Ser	Leu	Gly	Arg	Lys	Thr	Gln	Arg	Ser	Leu
				65					70					75
Leu	Ala	Glu	Leu	His	Val	Leu	Thr	Val	Lys	Glu	Ser	Asp	Ala	Gly
				80					85					90
Arg	Tyr	Tyr	Cys	Ala	Ala	Asp	Asn	Val	His	Ser	Pro	Ile	Leu	Ser
				95					100					105
Thr	Trp	Ile	Arg	Val	Thr	Val	Arg	Ile	Pro	Val	Ser	His	Pro	Val
				110					115					120
Leu	Thr	Phe	Arg	Ala	Pro	Arg	Ala	His	Thr	Val	Val	Gly	Asp	Leu
				125					130					135
Leu	Glu	Leu	His	Cys	Glu	Ser	Leu	Arg	Gly	Ser	Pro	Pro	Ile	Leu
				140					145					150
Tyr	Arg	Phe	Tyr	His	Glu	Asp	Val	Thr	Leu	Gly	Asn	Ser	Ser	Ala
				155					160					165
Pro	Ser	Gly	Gly	Gly	Ala	Ser	Phe	Asn	Leu	Ser	Leu	Thr	Ala	Glu
				170					175					180
His	Ser	Gly	Asn	Tyr	Ser	Cys	Asp	Ala	Asp	Asn	Gly	Leu	Gly	Ala
				185					190					195
Gln	His	Ser	His	Gly	Val	Ser	Leu	Arg	Val	Thr	Val	Pro	Val	Ser
				200					205					210
Arg	Pro	Val	Leu	Thr	Leu	Arg	Ala	Pro	Gly	Ala	Gln	Ala	Val	Val
				215					220					225
Gly	Asp	Leu	Leu	Glu	Leu	His	Cys	Glu	Ser	Leu	Arg	Gly	Ser	Phe
				230					235					240
Pro	Ile	Leu	Tyr	Trp	Phe	Tyr	His	Glu	Asp	Asp	Thr	Leu	Gly	Asn
				245					250					255
Ile	Ser	Ala	His	Ser	Gly	Gly	Gly	Ala	Ser	Phe	Asn	Leu	Ser	Leu
				260					265					270
Thr	Thr	Glu	His	Ser	Gly	Asn	Tyr	Ser	Cys	Glu	Ala	Asp	Asn	Gly
				275					280					285
Leu	Gly	Ala	Gln	His	Ser	Lys	Val	Val	Thr	Leu	Asn	Val	Thr	Gly
				290					295					300
Thr	Ser	Arg	Asn	Arg	Thr	Gly	Leu	Thr	Ala	Ala	Gly	Ile	Thr	Gly
				305					310					315
Leu	Val	Leu	Ser	Ile	Leu	Val	Leu	Ala	Ala	Ala	Ala	Ala	Leu	Leu
				320					325					330
His	Tyr	Ala	Arg	Ala	Arg	Arg	Lys	Pro	Gly	Gly	Leu	Ser	Ala	Thr
				335					340					345

Gly	Thr	Ser	Ser	His	Ser	Pro	Ser	Glu	Cys	Gln	Glu	Pro	Ser	Ser	
				350					355					360	
Ser	Arg	Pro	Ser	Arg	Ile	Asp	Pro	Gln	Glu	Pro	Thr	His	Ser	Lys	
				365					370					375	
Pro	Leu	Ala	Pro	Met	Glu	Leu	Glu	Pro	Met	Tyr	Ser	Asn	Val	Asn	
				380					385					390	
Pro	Gly	Asp	Ser	Asn	Pro	Ile	Tyr	Ser	Gln	Ile	Trp	Ser	Ile	Gln	
				395					400					405	
His	Thr	Lys	Glu	Asn	Ser	Ala	Asn	Cys	Pro	Met	Met	His	Gln	Glu	
				410					415					420	
His	Glu	Glu	Leu	Thr	Val	Leu	Tyr	Ser	Glu	Leu	Lys	Lys	Thr	His	
				425					430					435	
Pro	Asp	Asp	Ser	Ala	Gly	Glu	Ala	Ser	Ser	Arg	Gly	Arg	Ala	His	
				440					445					450	
Glu	Glu	Asp	Asp	Glu	Glu	Asn	Tyr	Glu	Asn	Val	Pro	Arg	Val	Leu	
				455					460					465	
Leu	Ala	Ser	Asp	His											
				470											

&lt;210&gt; 177

&lt;211&gt; 938

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:407346.1.orf3:2002JAN18

&lt;400&gt; 177

Arg	Leu	Glu	Thr	Ala	Leu	Lys	Phe	Leu	Glu	Gly	Arg	Lys	Ser	Met	
1				5					10					15	
His	Arg	Gly	Ser	Pro	Ile	Lys	Leu	Val	Asn	Ile	Asn	Ser	Thr	Asp	
				20					25					30	
Ile	Ala	Asp	Gly	Arg	Pro	Ser	Ile	Val	Leu	Gly	Leu	Met	Trp	Thr	
				35					40					45	
Ile	Ile	Leu	Tyr	Phe	Gln	Ile	Glu	Glu	Leu	Thr	Ser	Asn	Leu	Pro	
				50					55					60	
Gln	Leu	Gln	Ser	Leu	Ser	Ser	Ser	Ala	Ser	Ser	Val	Asp	Ser	Ile	
				65					70					75	
Val	Ser	Ser	Glu	Thr	Pro	Ser	Pro	Pro	Ser	Lys	Arg	Lys	Val	Thr	
				80					85					90	
Thr	Lys	Ile	Gln	Gly	Asn	Ala	Lys	Lys	Ala	Leu	Leu	Lys	Trp	Val	
				95					100					105	
Gln	Tyr	Thr	Ala	Gly	Lys	Gln	Thr	Gly	Ile	Glu	Val	Lys	Asp	Phe	
				110					115					120	
Gly	Lys	Ser	Trp	Arg	Ser	Gly	Val	Ala	Phe	His	Ser	Val	Ile	His	
				125					130					135	
Ala	Ile	Arg	Pro	Glu	Leu	Val	Asp	Leu	Glu	Thr	Val	Lys	Gly	Arg	
				140					145					150	
Ser	Asn	Arg	Glu	Asn	Leu	Glu	Asp	Ala	Phe	Thr	Ile	Ala	Glu	Thr	
				155					160					165	
Glu	Leu	Gly	Ile	Pro	Arg	Leu	Leu	Asp	Pro	Glu	Asp	Val	Asp	Val	
				170					175					180	
Asp	Lys	Pro	Asp	Glu	Lys	Ser	Ile	Met	Thr	Tyr	Val	Ala	Gln	Phe	
				185					190					195	
Leu	Lys	His	Tyr	Pro	Asp	Ile	His	Asn	Ala	Ser	Thr	Asp	Gly	Gln	
				200					205					210	
Glu	Asp	Asp	Glu	Ile	Leu	Pro	Gly	Phe	Pro	Ser	Phe	Ala	Asn	Ser	
				215					220					225	
Val	Gln	Asn	Phe	Lys	Arg	Glu	Asp	Arg	Val	Ile	Phe	Lys	Glu	Met	
				230					235					240	
Lys	Val	Trp	Ile	Glu	Gln	Phe	Glu	Arg	Asp	Leu	Thr	Arg	Ala	Gln	
				245					250					255	

Met	Val	Glu	Ser	Asn	Leu	Gln	Asp	Lys	Tyr	Gln	Ser	Phe	Lys	His
				260					265					270
Phe	Arg	Val	Gln	Tyr	Glu	Met	Lys	Arg	Lys	Gln	Ile	Glu	His	Leu
				275					280					285
Ile	Gln	Pro	Leu	His	Arg	Asp	Gly	Lys	Leu	Ser	Leu	Asp	Gln	Ala
				290					295					300
Leu	Val	Lys	Gln	Ser	Trp	Asp	Arg	Val	Thr	Ser	Arg	Leu	Phe	Asp
				305					310					315
Trp	His	Ile	Gln	Leu	Asp	Lys	Ser	Leu	Pro	Ala	Pro	Leu	Gly	Thr
				320					325					330
Ile	Gly	Ala	Trp	Leu	Tyr	Arg	Ala	Glu	Val	Ala	Leu	Arg	Glu	Glu
				335					340					345
Ile	Thr	Val	Gln	Gln	Val	His	Glu	Glu	Thr	Ala	Asn	Thr	Ile	Gln
				350					355					360
Arg	Lys	Leu	Glu	Gln	His	Lys	Asp	Leu	Leu	Gln	Asn	Thr	Asp	Ala
				365					370					375
His	Lys	Arg	Ala	Phe	His	Glu	Ile	Tyr	Arg	Thr	Arg	Ser	Val	Asn
				380					385					390
Gly	Ile	Pro	Val	Pro	Pro	Asp	Gln	Leu	Glu	Asp	Met	Ala	Glu	Arg
				395					400					405
Phe	His	Phe	Val	Ser	Ser	Thr	Ser	Glu	Leu	His	Leu	Met	Lys	Met
				410					415					420
Glu	Phe	Leu	Glu	Leu	Lys	Tyr	Arg	Leu	Leu	Ser	Leu	Leu	Val	Leu
				425					430					435
Ala	Glu	Ser	Lys	Leu	Lys	Ser	Trp	Ile	Ile	Lys	Tyr	Gly	Arg	Arg
				440					445					450
Glu	Ser	Val	Glu	Gln	Leu	Leu	Gln	Asn	Tyr	Val	Ser	Phe	Ile	Glu
				455					460					465
Asn	Ser	Lys	Phe	Phe	Glu	Gln	Tyr	Glu	Val	Thr	Tyr	Gln	Ile	Leu
				470					475					480
Lys	Gln	Thr	Ala	Glu	Met	Tyr	Val	Lys	Ala	Asp	Gly	Ser	Val	Glu
				485					490					495
Glu	Ala	Glu	Asn	Val	Met	Lys	Phe	Met	Asn	Glu	Thr	Thr	Ala	Gln
				500					505					510
Trp	Arg	Asn	Leu	Ser	Val	Glu	Val	Arg	Ser	Val	Arg	Ser	Met	Leu
				515					520					525
Glu	Glu	Val	Ile	Ser	Asn	Trp	Asp	Arg	Tyr	Gly	Asn	Thr	Val	Ala
				530					535					540
Ser	Leu	Gln	Ala	Trp	Leu	Glu	Asp	Ala	Glu	Lys	Met	Leu	Asn	Gln
				545					550					555
Ser	Glu	Asn	Ala	Lys	Lys	Asp	Phe	Phe	Arg	Asn	Leu	Pro	His	Trp
				560					565					570
Ile	Gln	Gln	His	Thr	Ala	Met	Asn	Asp	Ala	Gly	Asn	Phe	Leu	Ile
				575					580					585
Glu	Thr	Cys	Asp	Glu	Met	Val	Ser	Arg	Asp	Leu	Lys	Gln	Gln	Leu
				590					595					600
Leu	Leu	Leu	Asn	Gly	Arg	Trp	Arg	Glu	Leu	Phe	Met	Glu	Val	Lys
				605					610					615
Gln	Tyr	Ala	Gln	Ala	Asp	Glu	Met	Asp	Arg	Met	Lys	Lys	Glu	Tyr
				620					625					630
Thr	Asp	Cys	Val	Val	Thr	Leu	Ser	Ala	Phe	Ala	Thr	Glu	Ala	His
				635					640					645
Lys	Lys	Leu	Ser	Glu	Pro	Leu	Glu	Val	Ser	Phe	Met	Asn	Val	Lys
				650					655					660
Leu	Leu	Ile	Gln	Asp	Leu	Glu	Asp	Ile	Glu	Gln	Arg	Val	Pro	Val
				665					670					675
Met	Asp	Ala	Gln	Tyr	Lys	Ile	Ile	Thr	Lys	Thr	Ala	His	Leu	Ile
				680					685					690
Thr	Lys	Glu	Ser	Pro	Gln	Glu	Glu	Gly	Lys	Glu	Met	Phe	Ala	Thr
				695					700					705
Met	Ser	Lys	Leu	Lys	Glu	Gln	Leu	Thr	Lys	Val	Lys	Glu	Cys	Tyr
				710					715					720
Ser	Pro	Leu	Leu	Tyr	Glu	Ser	Gln	Gln	Leu	Leu	Ile	Pro	Leu	Glu

				725					730					735
Glu	Leu	Glu	Lys	Gln	Met	Thr	Ser	Phe	Tyr	Asp	Ser	Leu	Gly	Lys
				740					745					750
Ile	Asn	Glu	Ile	Ile	Thr	Val	Leu	Glu	Arg	Glu	Ala	Gln	Ser	Ser
				755					760					765
Ala	Leu	Phe	Lys	Gln	Lys	His	Gln	Glu	Leu	Leu	Ala	Cys	Gln	Glu
				770					775					780
Asn	Cys	Lys	Lys	Thr	Leu	Thr	Leu	Ile	Glu	Lys	Gly	Ser	Gln	Ser
				785					790					795
Val	Gln	Lys	Phe	Val	Thr	Leu	Ser	Asn	Val	Leu	Lys	His	Phe	Asp
				800					805					810
Gln	Thr	Arg	Leu	Gln	Arg	Gln	Ile	Ala	Asp	Ile	His	Val	Ala	Phe
				815					820					825
Gln	Ser	Met	Val	Lys	Lys	Thr	Gly	Asp	Trp	Lys	Lys	His	Val	Glu
				830					835					840
Thr	Asn	Ser	Arg	Leu	Met	Lys	Lys	Phe	Glu	Glu	Ser	Arg	Ala	Glu
				845					850					855
Leu	Glu	Lys	Val	Leu	Arg	Ile	Ala	Gln	Glu	Gly	Leu	Glu	Glu	Lys
				860					865					870
Gly	Asp	Pro	Glu	Glu	Leu	Leu	Arg	Arg	His	Thr	Glu	Phe	Phe	Ser
				875					880					885
Gln	Leu	Asp	Gln	Arg	Val	Leu	Asn	Ala	Phe	Leu	Lys	Ala	Cys	Asp
				890					895					900
Glu	Leu	Thr	Asp	Ile	Phe	Gln	Ser	Arg	Ser	Ser	Arg	Gly	Cys	Arg
				905					910					915
Lys	Leu	Phe	Glu	Ser	Ser	Thr	Asn	Asn	Gly	Arg	Ile	Phe	Lys	Glu
				920					925					930
Lys	Pro	Leu	Ile	Ile	Cys	Phe	Ile							
				935										

&lt;210&gt; 178

&lt;211&gt; 928

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:407689.7.orf3:2002JAN18

&lt;400&gt; 178

Ser	Gly	Tyr	Gly	Arg	Lys	Cys	Leu	Glu	Val	Leu	Asn	Leu	Gly	Val
1				5					10					15
Leu	Asn	Arg	Met	Asn	His	Ile	Lys	His	Val	Asp	Leu	Arg	Met	Asn
				20					25					30
His	Leu	Lys	Thr	Met	Val	Ile	Glu	Asn	Leu	Glu	Gly	Asn	Lys	His
				35					40					45
Ile	Thr	His	Val	Asp	Leu	Arg	Asp	Asn	Arg	Leu	Thr	Asp	Leu	Asp
				50					55					60
Leu	Ser	Ser	Leu	Cys	Ser	Leu	Glu	Gln	Leu	His	Cys	Gly	Arg	Asn
				65					70					75
Gln	Leu	Arg	Glu	Leu	Thr	Leu	Ser	Gly	Phe	Ser	Leu	Arg	Thr	Leu
				80					85					90
Tyr	Ala	Ser	Ser	Asn	Arg	Leu	Thr	Ala	Val	Asn	Val	Tyr	Pro	Val
				95					100					105
Pro	Ser	Leu	Leu	Thr	Phe	Leu	Asp	Leu	Ser	Arg	Asn	Leu	Leu	Glu
				110					115					120
Cys	Val	Pro	Asp	Trp	Ala	Cys	Glu	Ala	Lys	Lys	Ile	Glu	Val	Leu
				125					130					135
Asp	Val	Ser	Tyr	Asn	Leu	Leu	Thr	Glu	Val	Pro	Val	Arg	Ile	Leu
				140					145					150
Ser	Ser	Leu	Ser	Leu	Arg	Lys	Leu	Met	Leu	Gly	His	Asn	His	Val
				155					160					165
Gln	Asn	Leu	Pro	Thr	Leu	Val	Glu	His	Ile	Pro	Leu	Glu	Val	Leu



170	175	180
Asp Leu Gln His Asn Ala Leu Thr Arg	Leu Pro Asp Thr Leu Phe	
185	190	195
Ser Lys Ala Leu Asn Leu Arg Tyr Leu	Asn Ala Ser Ala Asn Ser	
200	205	210
Leu Glu Ser Leu Pro Ser Ala Cys Thr	Gly Glu Glu Ser Leu Ser	
215	220	225
Met Leu Gln Leu Leu Tyr Leu Thr Asn	Asn Leu Leu Thr Asp Gln	
230	235	240
Cys Ile Pro Val Leu Val Gly His Leu	His Leu Arg Ile Leu His	
245	250	255
Leu Ala Asn Asn Gln Leu Gln Thr Phe	Pro Ala Ser Lys Leu Asn	
260	265	270
Lys Leu Glu Gln Leu Glu Glu Leu Asn	Leu Ser Gly Asn Lys Leu	
275	280	285
Lys Thr Ile Pro Thr Thr Ile Ala Asn	Cys Lys Arg Leu His Thr	
290	295	300
Leu Val Ala His Ser Asn Asn Ile Ser	Ile Phe Pro Glu Ile Leu	
305	310	315
Gln Leu Pro Gln Ile Gln Phe Val Asp	Leu Ser Cys Asn Asp Leu	
320	325	330
Thr Glu Ile Leu Ile Pro Glu Ala Leu	Pro Ala Thr Leu Gln Asp	
335	340	345
Leu Asp Leu Thr Gly Asn Thr Asn Leu	Val Leu Glu His Lys Thr	
350	355	360
Leu Asp Ile Phe Ser His Ile Thr Thr	Leu Lys Ile Asp Gln Lys	
365	370	375
Pro Leu Pro Thr Thr Asp Ser Thr Val	Thr Ser Thr Phe Trp Ser	
380	385	390
His Gly Leu Ala Glu Met Ala Gly Gln	Arg Asn Lys Leu Cys Val	
395	400	405
Ser Ala Leu Ala Met Asp Ser Phe Ala	Glu Gly Val Gly Ala Val	
410	415	420
Tyr Gly Met Phe Asp Gly Asp Arg Asn	Glu Glu Leu Pro Arg Leu	
425	430	435
Leu Gln Cys Thr Met Ala Asp Val Leu	Leu Glu Glu Val Gln Gln	
440	445	450
Ser Thr Asn Asp Thr Val Phe Met Ala	Asn Thr Phe Leu Val Ser	
455	460	465
His Arg Lys Leu Gly Met Ala Gly Gln	Lys Leu Gly Ser Ser Ala	
470	475	480
Leu Leu Cys Tyr Ile Arg Pro Asp Thr	Ala Asp Pro Ala Ser Ser	
485	490	495
Phe Ser Leu Thr Val Ala Asn Val Gly	Thr Cys Gln Ala Val Leu	
500	505	510
Cys Arg Gly Gly Lys Pro Val Pro Leu	Ser Lys Val Phe Ser Leu	
515	520	525
Glu Gln Asp Pro Glu Glu Ala Gln Arg	Val Lys Asp Gln Lys Ala	
530	535	540
Ile Ile Thr Glu Asp Asn Lys Val Asn	Gly Val Thr Cys Cys Thr	
545	550	555
Arg Met Leu Gly Cys Thr Tyr Leu Tyr	Pro Trp Ile Leu Pro Lys	
560	565	570
Pro His Ile Ser Ser Thr Pro Leu Thr	Ile Gln Asp Glu Leu Leu	
575	580	585
Ile Leu Gly Asn Lys Ala Leu Trp Glu	His Leu Ser Tyr Thr Glu	
590	595	600
Ala Val Asn Ala Val Arg His Val Gln	Asp Pro Leu Ala Ala Ala	
605	610	615
Lys Lys Leu Cys Thr Leu Ala Gln Ser	Tyr Gly Cys Gln Asp Asn	
620	625	630
Val Gly Ala Met Val Val Tyr Leu Asn	Ile Gly Glu Glu Gly Cys	
635	640	645

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Thr Cys Glu Met Asn Gly Leu Thr Leu Pro Gly Pro Val Gly Phe
650 655 660
Ala Ser Thr Thr Thr Ile Lys Asp Ala Pro Lys Pro Ala Thr Pro
665 670 675
Ser Ser Ser Ser Gly Ile Ala Ser Glu Phe Ser Ser Glu Met Ser
680 685 690
Thr Ser Glu Val Ser Ser Glu Val Gly Ser Thr Ala Ser Asp Glu
695 700 705
His Asn Ala Gly Gly Leu Asp Thr Ala Leu Leu Pro Arg Pro Glu
710 715 720
Arg Arg Cys Ser Leu His Pro Thr Pro Thr Ser Gly Leu Phe Gln
725 730 735
Arg Gln Pro Ser Ser Ala Thr Phe Ser Ser Asn Gln Ser Asp Asn
740 745 750
Gly Leu Asp Ser Asp Asp Asp Gln Pro Val Glu Gly Val Ile Thr
755 760 765
Asn Gly Ser Lys Val Glu Val Glu Val Asp Ile His Cys Cys Arg
770 775 780
Gly Arg Asp Leu Glu Asn Ser Pro Pro Leu Ile Glu Ser Ser Pro
785 790 795
Thr Leu Cys Ser Glu Glu His Ala Arg Gly Ser Cys Phe Gly Ile
800 805 810
Arg Arg Gln Asn Ser Val Asn Ser Gly Met Leu Leu Pro Met Ser
815 820 825
Lys Asp Arg Met Glu Leu Gln Lys Ser Pro Ser Thr Ser Cys Leu
830 835 840
Tyr Gly Lys Lys Leu Ser Asn Gly Ser Ile Val Pro Leu Glu Asp
845 850 855
Ser Leu Asn Leu Ile Glu Val Ala Thr Glu Val Pro Lys Arg Lys
860 865 870
Thr Gly Tyr Phe Ala Ala Pro Thr Gln Met Glu Pro Glu Asp Gln
875 880 885
Phe Val Val Pro His Asp Leu Glu Glu Glu Val Lys Glu Gln Met
890 895 900
Lys Gln His Gln Asp Ser Arg Leu Glu Pro Glu Pro His Glu Glu
905 910 915
Asp Arg Thr Glu Pro Pro Glu Glu Phe Asp Thr Ala Leu
920 925

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&lt;210&gt; 179

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:407700.1.orf2:2002JAN18

&lt;400&gt; 179

```

Pro Gly Pro Trp Ala Pro Ala Arg Ala Gly Ala Gly Ala Ser Gly
1 5 10 15
Met Ala Phe Arg Gln Ala Leu Gln Leu Ala Ala Cys Gly Leu Ala
20 25 30
Gly Gly Ser Ala Ala Val Leu Phe Ser Ala Val Ala Val Gly Lys
35 40 45
Pro Arg Ala Gly Gly Asp Ala Glu Pro Arg Pro Ala Glu Pro Pro
50 55 60
Ala Trp Ala Gly Gly Ala Arg Pro Gly Pro Gly Val Trp Asp Pro
65 70 75
Asn Trp Asp Arg Arg Glu Pro Leu Ser Leu Ile Asn Val Arg Lys
80 85 90
Arg Asn Val Glu Ser Gly Glu Glu Glu Leu Ala Ser Lys Leu Asp
95 100 105

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His Tyr Lys Ala Lys Ala Thr Arg His Ile Phe Leu Ile Arg His
110 115 120
Ser Gln Tyr His Val Asp Gly Ser Leu Glu Lys Asp Arg Thr Leu
125 130 135
Thr Pro Leu Gly Arg Glu Gln Ala Glu Leu Thr Gly Leu Arg Leu
140 145 150
Ala Ser Leu Gly Leu Lys Phe Asn Lys Ile Val His Ser Ser Met
155 160 165
Thr Arg Ala Ile Glu Thr Thr Asp Ile Ile Ser Arg His Leu Pro
170 175 180
Gly Val Cys Lys Val Ser Thr Asp Leu Leu Arg Glu Gly Ala Pro
185 190 195
Ile Glu Pro Asp Pro Pro Val Ser His Trp Lys Pro Glu Ala Val
200 205 210
Gln Tyr Tyr Glu Asp Gly Ala Arg Ile Glu Ala Ala Phe Arg Asn
215 220 225
Tyr Ile His Arg Ala Asp Ala Arg Gln Glu Glu Asp Ser Tyr Glu
230 235 240
Ile Phe Ile Cys His Ala Asn Val Ile Arg Tyr Ile Val Cys Arg
245 250 255
Ala Leu Gln Phe Pro Pro Glu Gly Trp Leu Arg Leu Ser Leu Asn
260 265 270
Asn Gly Ser Ile Thr His Leu Val Ile Arg Pro Asn Gly Arg Val
275 280 285
Ala Leu Arg Thr Leu Gly Asp Thr Gly Phe Met Pro Pro Asp Lys
290 295 300
Ile Thr Arg Ser

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&lt;210&gt; 180

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:410461.92.orf3:2002JAN18

&lt;400&gt; 180

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Ala Pro Ala Pro Glu Pro Gly Pro Arg Ala Ala Ala Ala Ala Gly
1 5 10 15
Gly Thr Met Ser Cys Ala Gly Arg Ala Gly Pro Ala Arg Leu Ala
20 25 30
Ala Leu Ala Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp
35 40 45
Asn Ala Ser Gln Glu Tyr Tyr Thr Ala Leu Ile Asn Val Thr Val
50 55 60
Gln Glu Pro Gly Arg Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg
65 70 75
Gly Arg Tyr Gly Leu Asp Ser Pro Lys Ala Glu Val Arg Gly Gln
80 85 90
Val Leu Ala Pro Leu Pro Leu His Gly Val Ala Asp His Leu Gly
95 100 105
Cys Asp Pro Gln Thr Arg Phe Phe Val Pro Pro Asn Ile Lys Gln
110 115 120
Trp Ile Ala Leu Leu Gln Arg Gly Asn Cys Thr Phe Lys Glu Lys
125 130 135
Ile Ser Arg Ala Ala Phe His Asn Ala Val Ala Val Val Ile Tyr
140 145 150
Asn Asn Lys Ser Lys Glu Glu Pro Val Thr Met Thr His Pro Gly
155 160 165
Thr Gly Asp Ile Ile Ala Val Met Ile Thr Glu Leu Arg Gly Lys
170 175 180

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Asp	Ile	Leu	Ser	Tyr	Leu	Glu	Asn	Phe	Ser	Arg	Gly	Ser	Leu	Val	
				185					190					195	
Phe	Val	Ser	Ile	Ser	Phe	Ile	Val	Leu	Met	Ile	Ile	Ser	Ser	Ala	
				200					205					210	
Trp	Leu	Ile	Phe	Tyr	Phe	Ile	Gln	Lys	Ile	Arg	Tyr	Thr	Asn	Ala	
				215					220					225	
Arg	Asp	Arg	Asn	Gln	Arg	Arg	Leu	Gly	Asp	Ala	Ala	Lys	Lys	Ala	
				230					235					240	
Ile	Ser	Lys	Leu	Thr	Thr	Arg	Thr	Val	Lys	Lys	Gly	Asp	Lys	Glu	
				245					250					255	
Thr	Asp	Pro	Asp	Phe	Asp	His	Cys	Ala	Val	Cys	Ile	Glu	Ser	Tyr	
				260					265					270	
Lys	Gln	Asn	Asp	Val	Val	Arg	Ile	Leu	Pro	Cys	Lys	His	Val	Phe	
				275					280					285	
His	Lys	Ser	Cys	Val	Asp	Pro	Trp	Leu	Ser	Glu	His	Cys	Thr	Cys	
				290					295					300	
Pro	Met	Cys	Lys	Leu	Asn	Ile	Leu	Lys	Ala	Leu	Gly	Asn	Cys	Ala	
				305					310					315	
Glu	Phe	Ala	Met	Tyr											
				320											

&lt;210&gt; 181

&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:411043.3.orf2:2002JAN18

&lt;400&gt; 181

Asn	His	Cys	Pro	Thr	Arg	Ala	Met	Ile	Val	Gln	Arg	Val	Val	Leu	
1				5					10					15	
Asn	Ser	Arg	Pro	Gly	Lys	Asn	Gly	Asn	Pro	Val	Ala	Glu	Asn	Phe	
				20					25					30	
Arg	Met	Glu	Glu	Val	Tyr	Leu	Pro	Asp	Asn	Ile	Asn	Glu	Gly	Gln	
				35					40					45	
Val	Gln	Val	Arg	Thr	Leu	Tyr	Leu	Ser	Val	Asp	Pro	Tyr	Met	Arg	
				50					55					60	
Cys	Arg	Met	Asn	Glu	Asp	Thr	Gly	Thr	Asp	Tyr	Ile	Thr	Pro	Trp	
				65					70					75	
Gln	Leu	Ser	Gln	Val	Val	Asp	Gly	Gly	Gly	Ile	Gly	Ile	Ile	Glu	
				80					85					90	
Glu	Ser	Lys	His	Thr	Asn	Leu	Thr	Lys	Gly	Asp	Phe	Val	Thr	Ser	
				95					100					105	
Phe	Tyr	Trp	Pro	Trp	Gln	Thr	Lys	Val	Ile	Leu	Asp	Gly	Asn	Ser	
				110					115					120	
Leu	Glu	Lys	Val	Asp	Pro	Gln	Leu	Val	Asp	Gly	His	Leu	Ser	Tyr	
				125					130					135	
Phe	Leu	Gly	Ala	Ile	Gly	Met	Pro	Gly	Leu	Thr	Ser	Leu	Ile	Gly	
				140					145					150	
Ile	Gln	Glu	Lys	Gly	His	Ile	Thr	Ala	Gly	Ser	Asn	Lys	Thr	Met	
				155					160					165	
Val	Val	Ser	Gly	Ala	Ala	Gly	Ala	Cys	Gly	Ser	Val	Ala	Gly	Gln	
				170					175					180	
Ile	Gly	His	Phe	Leu	Gly	Cys	Ser	Arg	Val	Val	Gly	Ile	Cys	Gly	
				185					190					195	
Thr	His	Glu	Lys	Cys	Ile	Leu	Leu	Thr	Ser	Glu	Leu	Gly	Phe	Asp	
				200					205					210	
Ala	Ala	Ile	Asn	Tyr	Lys	Lys	Asp	Asn	Val	Ala	Glu	Gln	Leu	Arg	
				215					220					225	
Glu	Ser	Cys	Pro	Ala	Gly	Val	Asp	Val	Tyr	Phe	Asp	Asn	Val	Gly	
				230					235					240	

Gly	Asn	Ile	Ser	Asp	Thr	Val	Ile	Ser	Gln	Met	Asn	Glu	Asn	Ser	245	250	255
His	Ile	Ile	Leu	Cys	Gly	Gln	Ile	Ser	Gln	Tyr	Asn	Lys	Asp	Val	260	265	270
Pro	Tyr	Pro	Pro	Pro	Leu	Ser	Pro	Ala	Ile	Glu	Ala	Ile	Gln	Lys	275	280	285
Glu	Arg	Asn	Ile	Thr	Arg	Glu	Arg	Phe	Leu	Val	Leu	Asn	Tyr	Lys	290	295	300
Asp	Lys	Phe	Glu	Pro	Gly	Ile	Leu	Gln	Leu	Ser	Gln	Trp	Phe	Lys	305	310	315
Glu	Gly	Lys	Leu	Lys	Ile	Lys	Glu	Thr	Val	Ile	Asn	Gly	Leu	Glu	320	325	330
Asn	Met	Gly	Ala	Ala	Phe	Gln	Ser	Met	Met	Thr	Gly	Gly	Asn	Ile	335	340	345
Gly	Lys	Gln	Ile	Val	Cys	Ile	Ser	Glu	Glu	Ile	Ser	Leu			350	355	

&lt;210&gt; 182

&lt;211&gt; 438

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:438690.47.orf1:2002JAN18

&lt;400&gt; 182

Arg	Val	Arg	Ala	Gly	Leu	Pro	Cys	Pro	Met	Cys	Ser	Gly	Arg	Phe	1	5	10	15
Gln	Asn	Ile	Gln	Val	Asn	Pro	Asp	Phe	Pro	Arg	Gly	Arg	Ile	Ser	20	25	30	35
Asn	Ser	Phe	Arg	Arg	Thr	Ser	Ser	Thr	Glu	Asn	Lys	Thr	Lys	Thr	40	45	50	55
Leu	Gly	Lys	Leu	His	Gln	Glu	Pro	Arg	Gln	Leu	Gln	Ser	Asp	Gly	60	65	70	75
Lys	Arg	Lys	Ile	Leu	Leu	Glu	Glu	Leu	Ala	Asn	Ser	Asp	Pro	Lys	80	85	90	95
Leu	Ala	Leu	Thr	Gly	Val	Pro	Ile	Val	Gln	Trp	Pro	Lys	Arg	Asp	100	105	110	115
Lys	Leu	Lys	Phe	Pro	Thr	Arg	Pro	Lys	Val	Arg	Val	Pro	Thr	Ile	120	125	130	135
Pro	Ile	Thr	Lys	Pro	His	Thr	Met	Lys	Pro	Ala	Pro	Arg	Leu	Thr	140	145	150	155
Pro	Val	Arg	Pro	Ala	Ala	Ala	Ser	Pro	Ile	Val	Ser	Gly	Ala	Arg	160	165	170	175
Arg	Arg	Arg	Val	Arg	Cys	Arg	Lys	Cys	Lys	Ala	Cys	Val	Gln	Gly	180	185	190	195
Glu	Cys	Gly	Val	Cys	His	Tyr	Cys	Arg	Asp	Met	Lys	Lys	Phe	Gly	200	205	210	215
Gly	Pro	Gly	Arg	Met	Lys	Gln	Ser	Cys	Val	Leu	Arg	Gln	Cys	Leu	220	225	230	235
Ala	Pro	Arg	Leu	Pro	His	Ser	Val	Thr	Cys	Ser	Leu	Cys	Gly	Glu	240	245	250	255
Val	Asp	Gln	Asn	Glu	Glu	Thr	Gln	Asp	Phe	Glu	Lys	Lys	Leu	Met	260	265	270	275
Glu	Cys	Cys	Ile	Cys	Asn	Glu	Ile	Val	His	Pro	Gly	Cys	Leu	Gln	280	285	290	295
Met	Asp	Gly	Glu	Gly	Leu	Leu	Asn	Glu	Glu	Leu	Pro	Asn	Cys	Trp	300	305	310	315
Glu	Cys	Pro	Lys	Cys	Tyr	Gln	Glu	Asp	Ser	Ser	Glu	Lys	Ala	Gln	320	325	330	335
Lys	Arg	Lys	Met	Glu	Glu	Ser	Asp	Glu	Glu	Ala	Val	Gln	Ala	Lys	340	345	350	355

Val	Leu	Arg	Pro	Leu	Arg	Ser	Cys	Asp	Glu	Pro	Leu	Thr	Pro	Pro
				275					280					285
Pro	His	Ser	Pro	Thr	Ser	Met	Leu	Gln	Leu	Ile	His	Asp	Pro	Val
				290					295					300
Ser	Pro	Arg	Gly	Met	Val	Thr	Arg	Ser	Ser	Pro	Gly	Ala	Gly	Pro
				305					310					315
Ser	Asp	His	His	Ser	Ala	Ser	Arg	Asp	Glu	Arg	Phe	Lys	Arg	Arg
				320					325					330
Gln	Leu	Leu	Arg	Leu	Gln	Ala	Thr	Glu	Arg	Thr	Met	Val	Arg	Glu
				335					340					345
Lys	Glu	Asn	Asn	Pro	Ser	Gly	Lys	Lys	Glu	Leu	Ser	Glu	Val	Glu
				350					355					360
Lys	Ala	Lys	Ile	Arg	Gly	Ser	Tyr	Leu	Thr	Val	Thr	Leu	Gln	Arg
				365					370					375
Pro	Thr	Lys	Glu	Leu	His	Gly	Thr	Ser	Ile	Val	Pro	Lys	Leu	Gln
				380					385					390
Ala	Ile	Thr	Ala	Ser	Ser	Ala	Asn	Leu	Arg	His	Ser	Pro	Arg	Val
				395					400					405
Leu	Val	Gln	His	Cys	Pro	Ala	Arg	Thr	Pro	Gln	Arg	Gly	Asp	Glu
				410					415					420
Glu	Gly	Leu	Gly	Gly	Ser	Arg	Arg	Arg	Lys	Arg	Arg	Arg	Arg	Asp
				425					430					435
Gly	Gly	Arg												

&lt;210&gt; 183

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No.: LG:444677.81.orf1:2002JAN18

&lt;400&gt; 183

Gln	Ala	Leu	Met	Leu	Val	Ser	Gly	Arg	Arg	Arg	Leu	Leu	Thr	Ala
1				5					10					15
Leu	Leu	Gln	Ala	Gln	Lys	Trp	Pro	Phe	Gln	Pro	Ser	Arg	Asp	Met
				20					25					30
Arg	Leu	Val	Gln	Phe	Arg	Ala	Pro	His	Leu	Val	Gly	Pro	His	Leu
				35					40					45
Gly	Leu	Glu	Thr	Gly	Asn	Gly	Gly	Gly	Val	Ile	Asn	Leu	Asn	Ala
				50					55					60
Phe	Asp	Pro	Thr	Leu	Pro	Lys	Thr	Met	Thr	Gln	Phe	Leu	Glu	Gln
				65					70					75
Gly	Glu	Ala	Thr	Leu	Ser	Val	Ala	Arg	Arg	Ala	Leu	Ala	Ala	Gln
				80					85					90
Leu	Pro	Val	Leu	Pro	Trp	Ser	Glu	Val	Thr	Phe	Leu	Ala	Pro	Val
				95					100					105
Thr	Trp	Pro	Asp	Lys	Val	Val	Cys	Val	Gly	Met	Asn	Tyr	Val	Asp
				110					115					120
His	Cys	Lys	Glu	Gln	Asn	Val	Pro	Val	Pro	Lys	Glu	Pro	Ile	Ile
				125					130					135
Phe	Ser	Lys	Phe	Ala	Ser	Ser	Ile	Val	Gly	Pro	Tyr	Asp	Glu	Val
				140					145					150
Val	Leu	Pro	Pro	Gln	Ser	Gln	Glu	Val	Asp	Trp	Glu	Val	Glu	Leu
				155					160					165
Ala	Val	Val	Ile	Gly	Lys	Lys	Gly	Lys	His	Ile	Lys	Ala	Thr	Asp
				170					175					180
Ala	Met	Ala	His	Val	Ala	Gly	Phe	Thr	Val	Ala	His	Asp	Val	Ser
				185					190					195
Ala	Arg	Asp	Trp	Leu	Thr	Arg	Arg	Asn	Gly	Lys	Gln	Trp	Leu	Leu
				200					205					210

Gly Lys Thr Phe Asp Thr Phe Cys Pro Leu Gly Pro Ala Leu Val  
 215 220 225  
 Thr Lys Asp Ser Val Ala Gly Arg Ser Leu Val Pro Ala Pro Trp  
 230 235 240  
 Tyr Leu Pro Leu His Arg  
 245

<210> 184

<211> 266

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Incyte ID No: LG:457464.24.orf3:2002JAN18

<400> 184

Gln Phe Ser Glu Gln Gln Pro Ser Tyr Gly Gly Gln Gln Gln Ser  
 1 5 10 15  
 Tyr Gly Gln Gln Gln Ser Tyr Asn Pro Pro Gln Gly Tyr Gly Gln  
 20 25 30  
 Gln Asn Gln Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly  
 35 40 45  
 Gly Gly Gly Asn Tyr Gly Gln Asp Gln Ser Ser Met Ser Ser Gly  
 50 55 60  
 Gly Gly Ser Gly Gly Gly Tyr Gly Asn Gln Asp Gln Ser Gly Gly  
 65 70 75  
 Gly Gly Ser Gly Gly Tyr Gly Gln Gln Asp Arg Gly Gly Arg Gly  
 80 85 90  
 Arg Gly Gly Ser Gly Gly Ala Ala Ala Ala Ala Val Val Val Thr  
 95 100 105  
 Thr Ala Ala Val Val Ala Met Asn Pro Glu Val Val Glu Val Ala  
 110 115 120  
 Val Glu Ala Glu Val Ala Trp Gly Pro Arg Asp Gln Gly Ser Arg  
 125 130 135  
 His Asp Ser Glu Gln Asp Asn Ser Asp Asn Asn Thr Ile Phe Val  
 140 145 150  
 Gln Gly Leu Gly Glu Asn Val Thr Ile Glu Ser Val Ala Asp Tyr  
 155 160 165  
 Phe Lys Gln Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Gln  
 170 175 180  
 Pro Met Ile Asn Leu Tyr Thr Asp Arg Glu Thr Gly Lys Leu Lys  
 185 190 195  
 Gly Glu Ala Thr Val Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala  
 200 205 210  
 Ala Ile Asp Trp Phe Asp Gly Lys Glu Phe Ser Gly Asn Pro Ile  
 215 220 225  
 Lys Val Ser Phe Ala Thr Arg Arg Ala Asp Phe Asn Arg Gly Gly  
 230 235 240  
 Gly Asn Gly Arg Gly Gly Arg Gly Arg Gly Gly Pro Met Gly Arg  
 245 250 255  
 Gly Gly Tyr Gly Gly Gly Gly Ser Ala Gly Trp  
 260 265

<210> 185

<211> 539

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Incyte ID No: LG:7684793.15.orf3:2002JAN18

&lt;400&gt; 185

Lys	Leu	Gly	Ser	Met	Glu	Pro	Ala	Pro	Ala	Arg	Ser	Pro	Arg	Pro
1				5					10					15
Gln	Gln	Asp	Pro	Ala	Arg	Pro	Gln	Glu	Pro	Thr	Met	Pro	Pro	Pro
				20					25					30
Glu	Thr	Pro	Ser	Glu	Gly	Arg	Gln	Pro	Ser	Pro	Ser	Pro	Ser	Pro
				35					40					45
Thr	Glu	Arg	Ala	Pro	Ala	Ser	Glu	Glu	Glu	Phe	Gln	Phe	Leu	Arg
				50					55					60
Cys	Gln	Gln	Cys	Gln	Ala	Glu	Ala	Lys	Cys	Pro	Lys	Leu	Leu	Pro
				65					70					75
Cys	Leu	His	Thr	Leu	Cys	Ser	Gly	Cys	Leu	Glu	Ala	Ser	Gly	Met
				80					85					90
Gln	Cys	Pro	Ile	Cys	Gln	Ala	Pro	Trp	Pro	Leu	Gly	Ala	Asp	Thr
				95					100					105
Pro	Ala	Leu	Asp	Asn	Val	Phe	Phe	Glu	Ser	Leu	Gln	Arg	Arg	Leu
				110					115					120
Ser	Val	Tyr	Arg	Gln	Ile	Val	Asp	Ala	Gln	Ala	Val	Cys	Thr	Arg
				125					130					135
Cys	Lys	Glu	Ser	Ala	Asp	Phe	Trp	Cys	Phe	Glu	Cys	Glu	Gln	Leu
				140					145					150
Leu	Cys	Ala	Lys	Cys	Phe	Glu	Ala	His	Gln	Trp	Phe	Leu	Lys	His
				155					160					165
Glu	Ala	Arg	Pro	Leu	Ala	Glu	Leu	Arg	Asn	Gln	Ser	Val	Arg	Glu
				170					175					180
Phe	Leu	Asp	Gly	Thr	Arg	Lys	Thr	Asn	Asn	Ile	Phe	Cys	Ser	Asn
				185					190					195
Pro	Asn	His	Arg	Thr	Pro	Thr	Leu	Thr	Ser	Ile	Tyr	Cys	Arg	Gly
				200					205					210
Cys	Ser	Lys	Pro	Leu	Cys	Cys	Ser	Cys	Ala	Leu	Leu	Asp	Ser	Ser
				215					220					225
His	Ser	Glu	Leu	Lys	Cys	Asp	Ile	Ser	Ala	Glu	Ile	Gln	Gln	Arg
				230					235					240
Gln	Glu	Glu	Leu	Asp	Ala	Met	Thr	Gln	Ala	Leu	Gln	Glu	Gln	Asp
				245					250					255
Ser	Ala	Phe	Gly	Ala	Val	His	Ala	Gln	Met	His	Ala	Ala	Val	Gly
				260					265					270
Gln	Leu	Gly	Arg	Ala	Arg	Ala	Glu	Thr	Glu	Glu	Leu	Ile	Arg	Glu
				275					280					285
Arg	Val	Arg	Gln	Val	Val	Ala	His	Val	Arg	Ala	Gln	Glu	Arg	Glu
				290					295					300
Leu	Leu	Glu	Ala	Val	Asp	Ala	Arg	Tyr	Gln	Arg	Asp	Tyr	Glu	Glu
				305					310					315
Met	Ala	Ser	Arg	Leu	Gly	Arg	Leu	Asp	Ala	Val	Leu	Gln	Arg	Ile
				320					325					330
Arg	Thr	Gly	Ser	Ala	Leu	Val	Gln	Arg	Met	Lys	Cys	Tyr	Ala	Ser
				335					340					345
Asp	Gln	Glu	Val	Leu	Asp	Met	His	Gly	Phe	Leu	Arg	Gln	Ala	Leu
				350					355					360
Cys	Arg	Leu	Arg	Gln	Glu	Glu	Pro	Gln	Ser	Leu	Gln	Ala	Ala	Val
				365					370					375
Arg	Thr	Asp	Gly	Phe	Asp	Glu	Phe	Lys	Val	Arg	Leu	Gln	Asp	Leu
				380					385					390
Ser	Ser	Cys	Ile	Thr	Gln	Gly	Lys	Asp	Ala	Ala	Val	Ser	Lys	Lys
				395					400					405
Ala	Ser	Pro	Glu	Ala	Ala	Ser	Thr	Pro	Arg	Asp	Pro	Ile	Asp	Val
				410					415					420
Asp	Leu	Ala	Glu	Glu	Ala	Glu	Arg	Val	Lys	Ala	Gln	Val	Gln	Ala
				425					430					435
Leu	Gly	Leu	Ala	Glu	Ala	Gln	Pro	Met	Ala	Val	Val	Gln	Ser	Val
				440					445					450
Pro	Gly	Ala	His	Pro	Val	Pro	Val	Tyr	Ala	Phe	Ser	Ile	Lys	Gly
				455					460					465



Pro	Ser	Tyr	Gly	Glu	Asp	Val	Ser	Asn	Thr	Thr	Thr	Ala	Gln	Lys
				470					475					480
Arg	Lys	Cys	Ser	Gln	Thr	Gln	Cys	Pro	Arg	Lys	Val	Ile	Lys	Met
				485					490					495
Glu	Ser	Glu	Glu	Gly	Lys	Glu	Ala	Arg	Leu	Ala	Arg	Ser	Ser	Pro
				500					505					510
Glu	Gln	Pro	Arg	Pro	Ser	Thr	Ser	Lys	Ala	Val	Ser	Pro	Pro	His
				515					520					525
Leu	Asp	Gly	Pro	Pro	Ser	Pro	Arg	Ser	Pro	Val	Ile	Gly	Ser	
				530					535					

&lt;210&gt; 186

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:7687485.1.orf1:2002JAN18

&lt;400&gt; 186

Thr	Gln	Leu	Thr	Thr	Asn	Gln	Thr	Asn	Pro	Ser	Gly	Gln	Ile	Ser
1				5					10					15
Tyr	Glu	Cys	Gly	Gln	Cys	Gly	Arg	Tyr	Phe	Ile	Gln	Met	Ala	Asp
				20					25					30
Phe	His	Arg	His	Glu	Lys	Cys	His	Thr	Gly	Glu	Lys	Ser	Phe	Glu
				35					40					45
Cys	Lys	Glu	Cys	Gly	Lys	Tyr	Phe	Arg	Tyr	Asn	Ser	Leu	Leu	Ile
				50					55					60
Arg	His	Gln	Ile	Ile	His	Thr	Gly	Lys	Lys	Pro	Phe	Lys	Cys	Lys
				65					70					75
Glu	Cys	Gly	Lys	Gly	Leu	Ser	Ser	Asp	Thr	Ala	Leu	Ile	Gln	His
				80					85					90
Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys
				95					100					105
Gly	Lys	Ala	Phe	Ser	Ser	Ser	Ser	Val	Phe	Leu	Gln	His	Gln	Arg
				110					115					120
Phe	His	Thr	Gly	Glu	Lys	Leu	Tyr	Glu	Cys	Asn	Glu	Cys	Trp	Lys
				125					130					135
Thr	Phe	Ser	Cys	Ser	Ser	Ser	Phe	Thr	Val	His	Gln	Arg	Met	His
				140					145					150
Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Arg	Leu
				155					160					165
Ser	Ser	Asn	Thr	Ala	Leu	Thr	Gln	His	Gln	Arg	Ile	His	Thr	Gly
				170					175					180
Glu	Lys	Pro	Phe	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Asn	Gln
				185					190					195
Lys	Ile	Thr	Leu	Ile	Gln	His	Gln	Arg	Val	His	Thr	Gly	Glu	Lys
				200					205					210
Pro	Tyr	Glu	Cys	Lys	Val	Cys	Gly	Lys	Thr	Phe	Ser	Trp	Cys	Gly
				215					220					225
Arg	Phe	Ile	Leu	His	Gln	Lys	Leu	His	Thr	Gln	Lys	Thr	Pro	Val
				230					235					240

Gln Ala

&lt;210&gt; 187

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

<223> Incyte ID No: LG:7689661.4.orf2:2002JAN18

<400> 187

Asn	Val	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Arg	Val	Arg	Gly	Gln	Leu
1				5					10					15
Thr	Leu	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys
				20					25					30
Lys	Glu	Cys	Gly	Lys	Thr	Phe	Ser	Arg	Gly	Tyr	His	Leu	Ile	Leu
				35					40					45
His	His	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Glu
				50					55					60
Cys	Trp	Lys	Ala	Phe	Ser	Arg	Tyr	Ser	Gln	Leu	Ile	Ser	His	Gln
				65					70					75
Ser	Ile	His	Ile	Gly	Val	Lys	Pro	Tyr	Asp	Cys	Lys	Glu	Cys	Gly
				80					85					90
Lys	Ala	Phe	Arg	Leu	Leu	Ser	Gln	Leu	Thr	Gln	His	Gln	Ser	Ile
				95					100					105
His	Ile	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Lys	Glu	Cys	Gly	Lys	Ala
				110					115					120
Phe	Arg	Leu	Arg	Gln	Lys	Leu	Thr	Leu	His	Gln	Ser	Ile	His	Thr
				125					130					135
Gly	Glu	Lys	Pro	Phe	Glu	Cys	Lys	Glu	Cys	Arg	Lys	Ala	Phe	Arg
				140					145					150
Leu	Asn	Ser	Ser	Leu	Ile	Gln	His	Leu	Arg	Ile	His	Ser	Gly	Glu
				155					160					165
Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Lys	Lys	Ala	Phe	Arg	Gln	His
				170					175					180
Ser	His	Leu	Thr	His	His	Leu	Lys	Ile	His	Asn	Val	Lys	Ile	
				185					190					

<210> 188

<211> 149

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Incyte ID No: LG:7690373.1.orf1:2002JAN18

<400> 188

Lys	Asn	Ser	Tyr	Trp	Arg	Lys	Asn	Pro	Thr	Asn	Met	Lys	Asn	Val
1				5					10					15
Ala	Lys	Leu	Leu	Ile	Asn	Ser	Gln	Arg	Leu	Leu	Asn	Ile	Arg	Glu
				20					25					30
Phe	Val	Gln	Glu	Gly	Asn	Pro	Thr	Asn	Leu	Lys	Asn	Val	Ala	Ser
				35					40					45
Leu	Leu	Ala	Ile	Pro	Gln	Ser	Leu	Leu	Asn	Ile	His	Val	Ile	His
				50					55					60
Thr	Gly	Gly	Asn	Ser	Tyr	Asn	Cys	Val	Glu	Cys	Cys	Asn	Ala	Leu
				65					70					75
Asn	Gln	Ser	Leu	Arg	Leu	Thr	Thr	Tyr	Lys	Thr	Thr	His	Thr	Gly
				80					85					90
Glu	Lys	Pro	Cys	Met	Cys	Glu	Glu	Cys	Gly	Lys	Ala	Ser	Asn	Arg
				95					100					105
Ser	Ser	Ile	Leu	Lys	Arg	His	Lys	Leu	Ile	His	Thr	Gln	Glu	Arg
				110					115					120
Leu	Tyr	Lys	Pro	Glu	Arg	Cys	Asp	Asn	Ala	Phe	Gly	Asn	Thr	Ser
				125					130					135
Asp	Phe	Ser	Glu	Tyr	Lys	Arg	Asn	Arg	Thr	Asp	Glu	Lys	Ser	
				140					145					

<210> 189

<211> 268

<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte ID No: LG:7696560.1.orf3:2002JAN18

<400> 189  
Lys Val Ala Thr Met Arg Lys Leu Phe Ser Phe Gly Arg Arg Leu  
1 5 10 15  
Gly Gln Ala Leu Leu Asp Ser Met Asp Gln Glu Tyr Ala Gly Arg  
20 25 30  
Gly Tyr His Ile Arg Asp Trp Glu Leu Arg Lys Ile His Arg Ala  
35 40 45  
Ala Ile Lys Gly Asp Ala Ala Glu Val Glu His Cys Leu Thr Arg  
50 55 60  
Arg Phe Arg Asp Leu Asp Ala Arg Asp Arg Lys Asp Arg Thr Val  
65 70 75  
Leu His Leu Thr Cys Ala His Gly Arg Val Glu Val Val Thr Leu  
80 85 90  
Leu Leu Ser Arg Arg Cys Gln Ile Asn Ile Tyr Asp Arg Leu Asn  
95 100 105  
Arg Thr Pro Leu Met Lys Ala Val His Cys Gln Glu Glu Ala Cys  
110 115 120  
Ala Ile Ile Leu Leu Glu His Gly Ala Asn Pro Asn Ile Lys Asp  
125 130 135  
Ile Tyr Ser Asn Thr Ala Leu His Tyr Ala Val Tyr Asn Lys Gly  
140 145 150  
Thr Ser Leu Ala Glu Lys Leu Leu Ser His His Ala Asn Ile Glu  
155 160 165  
Ala Leu Asn Glu Glu Gly Asn Thr Pro Leu Leu Phe Ala Ile Asn  
170 175 180  
Ser Arg Arg Gln Gln Ile Val Glu Phe Leu Leu Lys Asn Gln Ala  
185 190 195  
Asn Leu His Ala Ile Asp Asn Phe Arg Arg Thr Ala Leu Met Leu  
200 205 210  
Ala Val Gln His Asn Ser Ser Ser Ile Val Ser Leu Leu Leu Gln  
215 220 225  
Gln Asn Ile Asn Ile Phe Ser Gln Asp Leu Phe Gly Gln Thr Ala  
230 235 240  
Glu Asp Tyr Ala Val Cys Tyr Asn Phe Arg Ser Ile Gln Gln Gln  
245 250 255  
Ile Leu Glu His Lys Asn Lys Ile Leu Lys Ser His Leu  
260 265

<210> 190  
<211> 1304  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte ID No: LG:7698190.26.orf3:2002JAN18

<220>  
<221> unsure  
<222> (1) ... (1304)  
<223> unknown or other

<400> 190  
Arg Trp Arg Lys Leu Pro Lys Met Pro Glu Ala Val Gly Thr Asp  
1 5 10 15  
Pro Ser Thr Ser Arg Lys Met Ala Glu Leu Glu Glu Val Thr Leu

	20		25		30
Asp Gly Lys Pro Leu	Gln Ala Leu Arg Val	Thr Asp Leu Lys Ala			
	35		40		45
Ala Leu Glu Gln Arg	Gly Leu Ala Lys Ser	Gly Gln Lys Ser Ala			
	50		55		60
Leu Val Lys Arg Leu	Lys Gly Ala Leu Met	Leu Glu Asn Leu Gln			
	65		70		75
Lys His Ser Thr Pro	His Ala Ala Phe Gln	Pro Asn Ser Gln Ile			
	80		85		90
Gly Glu Glu Met Ser	Gln Asn Ser Phe Ile	Lys Gln Tyr Leu Glu			
	95		100		105
Lys Gln Gln Glu Leu	Leu Arg Gln Arg Leu	Glu Arg Glu Ala Arg			
	110		115		120
Glu Ala Ala Glu Leu	Glu Glu Ala Ser Ala	Glu Ser Glu Asp Glu			
	125		130		135
Met Ile His Pro Glu	Gly Val Ala Ser Leu	Leu Pro Pro Asp Phe			
	140		145		150
Gln Ser Ser Leu Glu	Arg Pro Glu Leu Glu	Leu Ser Arg His Ser			
	155		160		165
Pro Arg Lys Ser Ser	Ser Ile Ser Glu Lys	Gly Asp Ser Asp			
	170		175		180
Asp Glu Lys Pro Arg	Lys Gly Glu Arg Arg	Ser Ser Arg Val Arg			
	185		190		195
Gln Ala Arg Ala Ala	Lys Leu Ser Glu Gly	Ser Gln Pro Ala Glu			
	200		205		210
Glu Glu Glu Asp Gln	Glu Thr Pro Ser Arg	Asn Leu Arg Val Arg			
	215		220		225
Ala Asp Arg Asn Leu	Lys Thr Glu Glu Glu	Glu Glu Glu Glu Asp			
	230		235		240
Gly Gly Gly Thr Lys	Ile Asp Glu Glu Glu	Gly Asp Asp Glu Gly			
	245		250		255
Gln Lys Ser Arg Glu	Ala Pro Ile Leu Lys	Glu Phe Lys Glu Glu			
	260		265		270
Gly Glu Glu Met Pro	Arg Val Lys Pro Glu	Glu Met Met Asp Glu			
	275		280		285
Arg Pro Lys Thr Arg	Ser Gln Glu Gln Glu	Val Leu Glu Arg Gly			
	290		295		300
Gly Arg Phe Thr Arg	Ser Gln Glu Glu Ala	Arg Lys Ser His Leu			
	305		310		315
Ala Arg Gln Gln Gln	Glu Lys Glu Met Lys	Thr Thr Ser Pro Leu			
	320		325		330
Glu Glu Glu Glu Arg	Glu Ile Lys Ser Ser	Gln Gly Leu Lys Glu			
	335		340		345
Lys Ser Lys Ser Pro	Ser Pro Pro Arg Leu	Thr Glu Asp Arg Lys			
	350		355		360
Lys Ala Ser Leu Val	Ala Leu Pro Glu Gln	Thr Ala Ser Glu Glu			
	365		370		375
Glu Thr Pro Pro Pro	Leu Leu Thr Lys Glu	Ala Ser Ser Pro Pro			
	380		385		390
Pro His Pro Gln Leu	His Ser Glu Glu Glu	Ile Glu Pro Met Glu			
	395		400		405
Gly Pro Ala Pro Pro	Val Leu Ile Gln Leu	Ser Pro Pro Asn Thr			
	410		415		420
Asp Ala Asp Thr Arg	Glu Leu Leu Val Ser	Gln His Thr Val Gln			
	425		430		435
Leu Val Gly Gly Leu	Ser Pro Leu Ser Ser	Pro Ser Asp Thr Lys			
	440		445		450
Ala Glu Ser Pro Ala	Glu Lys Val Pro Glu	Glu Ser Val Leu Pro			
	455		460		465
Leu Val Gln Lys Ser	Thr Leu Ala Asp Tyr	Ser Ala Gln Lys Asp			
	470		475		480
Leu Glu Pro Glu Ser	Asp Arg Ser Ala Gln	Pro Leu Pro Leu Lys			
	485		490		495

Ile	Glu	Glu	Leu	Ala	Leu	Ala	Lys	Gly	Ile	Thr	Glu	Glu	Cys	Leu
				500					505					510
Lys	Gln	Pro	Ser	Leu	Glu	Gln	Lys	Glu	Gly	Arg	Arg	Ala	Ser	His
				515					520					525
Thr	Leu	Leu	Pro	Ser	His	Arg	Leu	Lys	Gln	Ser	Ala	Asp	Ser	Ser
				530					535					540
Ser	Ser	Arg	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Arg	Ser	Arg
				545					550					555
Ser	Arg	Ser	Pro	Asp	Ser	Ser	Gly	Ser	Arg	Ser	His	Ser	Pro	Leu
				560					565					570
Arg	Ser	Lys	Gln	Arg	Asp	Val	Ala	Gln	Ala	Arg	Thr	His	Ala	Asn
				575					580					585
Pro	Arg	Gly	Arg	Pro	Lys	Met	Gly	Ser	Arg	Ser	Thr	Ser	Glu	Ser
				590					595					600
Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Ala	Ser	Ser	Asn	Ser
				605					610					615
Arg	Lys	Ser	Leu	Ser	Pro	Gly	Val	Ser	Arg	Asp	Ser	Ser	Thr	Ser
				620					625					630
Tyr	Thr	Glu	Thr	Lys	Asp	Pro	Ser	Ser	Gly	Gln	Glu	Val	Ala	Thr
				635					640					645
Pro	Pro	Val	Pro	Gln	Leu	Gln	Val	Cys	Glu	Pro	Lys	Glu	Arg	Thr
				650					655					660
Ser	Thr	Ser	Ser	Ser	Ser	Val	Gln	Ala	Arg	Arg	Leu	Ser	Gln	Pro
				665					670					675
Glu	Ser	Ala	Glu	Lys	His	Val	Thr	Gln	Arg	Leu	Gln	Pro	Glu	Arg
				680					685					690
Gly	Ser	Pro	Lys	Lys	Cys	Glu	Ala	Glu	Glu	Ala	Glu	Pro	Pro	Ala
				695					700					705
Ala	Thr	Gln	Pro	Gln	Thr	Ser	Glu	Thr	Gln	Thr	Ser	His	Leu	Pro
				710					715					720
Glu	Ser	Glu	Arg	Ile	His	His	Thr	Val	Glu	Glu	Lys	Glu	Glu	Val
				725					730					735
Thr	Met	Asp	Thr	Ser	Glu	Asn	Arg	Pro	Glu	Asn	Asp	Val	Pro	Glu
				740					745					750
Pro	Pro	Met	Pro	Ile	Ala	Asp	Gln	Val	Ser	Asn	Asp	Asp	Arg	Pro
				755					760					765
Glu	Gly	Ser	Val	Glu	Asp	Glu	Glu	Lys	Lys	Glu	Ser	Ser	Leu	Pro
				770					775					780
Lys	Ser	Phe	Lys	Arg	Lys	Ile	Ser	Val	Val	Ser	Ala	Thr	Lys	Gly
				785					790					795
Val	Pro	Ala	Gly	Asn	Ser	Asp	Thr	Glu	Gly	Gly	Gln	Pro	Gly	Arg
				800					805					810
Lys	Arg	Arg	Trp	Gly	Ala	Ser	Thr	Ala	Thr	Thr	Gln	Lys	Lys	Pro
				815					820					825
Ser	Ile	Ser	Ile	Thr	Thr	Glu	Ser	Leu	Lys	Ser	Leu	Ile	Pro	Asp
				830					835					840
Ile	Lys	Pro	Leu	Ala	Gly	Gln	Glu	Ala	Val	Val	Asp	Leu	His	Ala
				845					850					855
Asp	Asp	Ser	Arg	Ile	Ser	Glu	Asp	Glu	Thr	Glu	Arg	Asn	Gly	Asp
				860					865					870
Asp	Gly	Thr	His	Asp	Lys	Gly	Leu	Lys	Ile	Cys	Arg	Thr	Val	Thr
				875					880					885
Gln	Val	Val	Pro	Ala	Glu	Gly	Gln	Glu	Asn	Gly	Gln	Arg	Glu	Glu
				890					895					900
Glu	Glu	Glu	Glu	Lys	Glu	Pro	Glu	Ala	Glu	Pro	Pro	Val	Pro	Pro
				905					910					915
Gln	Val	Ser	Val	Glu	Val	Ala	Leu	Pro	Pro	Pro	Ala	Glu	His	Glu
				920					925					930
Val	Lys	Lys	Val	Thr	Leu	Gly	Asp	Thr	Leu	Thr	Arg	Arg	Ser	Ile
				935					940					945
Ser	Gln	Gln	Lys	Ser	Gly	Val	Ser	Ile	Thr	Ile	Asp	Asp	Pro	Val
				950					955					960
Arg	Thr	Ala	Gln	Val	Pro	Ser	Pro	Pro	Arg	Gly	Lys	Ile	Ser	Asn

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          965          970          975
Ile Val His Ile Ser Asn Leu Val Arg Pro Phe Thr Leu Gly Gln
          980          985          990
Leu Lys Glu Leu Leu Gly Arg Thr Gly Thr Leu Val Glu Glu Ala
          995          1000          1005
Phe Trp Ile Asp Lys Ile Lys Ser His Cys Phe Val Thr Tyr Ser
          1010          1015          1020
Thr Val Glu Glu Ala Val Ala Thr Arg Thr Ala Leu His Gly Val
          1025          1030          1035
Lys Trp Pro Gln Ser Asn Pro Lys Phe Leu Cys Ala Asp Tyr Ala
          1040          1045          1050
Glu Gln Asp Glu Leu Asp Tyr His Arg Gly Leu Leu Val Asp Arg
          1055          1060          1065
Pro Ser Glu Thr Lys Thr Glu Glu Gln Gly Ile Pro Arg Pro Leu
          1070          1075          1080
His Pro Pro Pro Pro Pro Pro Val Gln Pro Pro Gln His Pro Arg
          1085          1090          1095
Ala Glu Gln Arg Glu Gln Glu Arg Ala Val Arg Glu Gln Trp Ala
          1100          1105          1110
Glu Arg Glu Arg Glu Met Glu Arg Arg Glu Arg Thr Arg Ser Glu
          1115          1120          1125
Arg Glu Trp Asp Arg Asp Lys Val Arg Glu Gly Pro Arg Ser Arg
          1130          1135          1140
Ser Arg Ser Arg Asp Arg Arg Arg Lys Glu Arg Ala Lys Ser Lys
          1145          1150          1155
Glu Lys Lys Ser Glu Lys Lys Glu Lys Ala Gln Glu Glu Pro Pro
          1160          1165          1170
Ala Lys Leu Leu Asp Asp Leu Phe Arg Lys Thr Lys Ala Ala Pro
          1175          1180          1185
Cys Ile Tyr Trp Leu Pro Leu Thr Asp Ser Gln Ile Val Gln Lys
          1190          1195          1200
Glu Ala Glu Arg Ala Glu Arg Ala Lys Glu Arg Glu Lys Arg Arg
          1205          1210          1215
Lys Glu Gln Glu Glu Glu Glu Gln Lys Glu Arg Glu Lys Glu Ala
          1220          1225          1230
Glu Arg Glu Arg Asn Arg Gln Leu Glu Arg Glu Lys Arg Arg Glu
          1235          1240          1245
His Ser Arg Glu Arg Asp Arg Xaa Arg Xaa Arg Glu Arg Glu Arg
          1250          1255          1260
Asp Arg Gly Asp Arg Asp Arg Asp Arg Glu Arg Asp Arg Glu Arg
          1265          1270          1275
Gly Arg Glu Arg Asp Arg Arg Asp Thr Lys Arg His Ser Arg Ser
          1280          1285          1290
Arg Ser Arg Ser Thr Pro Val Arg Asp Arg Gly Gly Arg Arg
          1295          1300

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&lt;210&gt; 191

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:7763560.12.orf1:2002JAN18

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1) ... (239)

&lt;223&gt; unknown or other

&lt;400&gt; 191

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Ser Arg Cys Xaa Val Thr Arg Gly Ser Gln Ala Trp Leu Pro Leu
  1              5              10              15

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Leu Phe Thr Pro Leu Tyr Glu Ser Ser His Leu Glu Arg Pro Ala
      20      25      30
Leu Arg Pro Met Val Ala Ala Arg Trp Gly Ala Thr Val Gly Pro
      35      40      45
Gly Ala Val Trp Thr Gln Cys Tyr Gly Trp Gly Trp Pro Glu Pro
      50      55      60
Ala Trp Asp Ser Arg Glu Trp Arg Arg Val Val Gly Pro Gly Lys
      65      70      75
Arg Pro Arg Leu Leu Ala His Pro Leu Trp Ala Ser Leu Glu Leu
      80      85      90
Leu Phe Leu Val Ser Gln Glu Asp Thr Leu Ser Pro Gly Ala Val
      95     100     105
Gly Pro Arg Cys Val Gly Asp Pro Gly Ser Ala Leu Gly Pro Leu
     110     115     120
His Val Gly Asp Thr Gly Asn Ala Arg Ser Pro Pro Cys Phe Ser
     125     130     135
Pro His Leu Pro Ile Ser Thr Cys Gly Ala Arg Gly Ser Asp Pro
     140     145     150
Lys Ala Ala Ser His Pro Pro Ser Pro Ala Pro Pro Ala Leu Arg
     155     160     165
Ala Gln Gly Ala Ala Gln Pro Cys His Leu Cys Ser Ser Pro Ala
     170     175     180
Pro His Thr Asn Leu Gly Pro Gly Gly Pro Ala His Pro Gly Leu
     185     190     195
Arg Arg Pro Pro Pro Leu Val His Met Ala Ser Pro Ser Cys Arg
     200     205     210
Gly Ser Gly Cys Cys Pro His Arg Ala Gly Ser Leu Leu Arg Cys
     215     220     225
Ala Gly Lys Ala Gly Trp Cys Arg Gly Ala Arg Arg Gly Arg
     230     235

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&lt;210&gt; 192

&lt;211&gt; 837

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:7763587.20.orf2:2002JAN18

&lt;400&gt; 192

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Pro Ala Leu Leu Ser Leu Val Leu Pro Ser Gln Gly Glu Ala Pro
  1      5      10      15
Ala Glu Met Gly Ala Leu Leu Leu Glu Lys Glu Thr Arg Gly Ala
      20      25      30
Thr Glu Arg Val His Gly Ser Leu Gly Asp Thr Pro Arg Ser Glu
      35      40      45
Glu Thr Leu Pro Lys Ala Thr Pro Asp Ser Leu Glu Pro Ala Gly
      50      55      60
Pro Ser Ser Pro Ala Ser Val Thr Val Thr Val Gly Asp Glu Gly
      65      70      75
Ala Asp Thr Pro Val Gly Ala Thr Pro Leu Ile Gly Asp Glu Ser
      80      85      90
Glu Asn Leu Glu Gly Asp Gly Asp Leu Arg Gly Gly Arg Ile Leu
      95     100     105
Leu Gly His Ala Thr Lys Ser Phe Pro Ser Ser Pro Ser Lys Gly
     110     115     120
Gly Ser Cys Pro Ser Arg Ala Lys Met Ser Met Thr Gly Ala Gly
     125     130     135
Lys Ser Pro Pro Ser Val Gln Ser Leu Ala Met Arg Leu Leu Ser
     140     145     150
Met Pro Gly Ala Gln Gly Ala Ala Ala Ala Gly Ser Glu Pro Pro
     155     160     165

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Pro	Ala	Thr	Thr	Ser	Pro	Glu	Gly	Gln	Pro	Lys	Val	His	Arg	Ala	170
Arg	Lys	Thr	Met	Ser	Lys	Pro	Gly	Asn	Gly	Gln	Pro	Pro	Val	Pro	175
Glu	Lys	Arg	Pro	Pro	Glu	Ile	Gln	His	Phe	Arg	Met	Ser	Asp	Asp	185
Val	His	Ser	Leu	Gly	Lys	Val	Thr	Ser	Asp	Leu	Ala	Lys	Arg	Arg	190
Lys	Leu	Asn	Ser	Gly	Gly	Gly	Leu	Ser	Glu	Glu	Leu	Gly	Ser	Ala	195
Arg	Arg	Ser	Gly	Glu	Val	Thr	Leu	Thr	Lys	Gly	Asp	Pro	Gly	Ser	200
Leu	Glu	Glu	Trp	Glu	Thr	Val	Val	Gly	Asp	Asp	Phe	Ser	Leu	Tyr	205
Tyr	Asp	Ser	Tyr	Ser	Val	Asp	Glu	Arg	Val	Asp	Ser	Asp	Ser	Lys	215
Ser	Glu	Val	Glu	Ala	Leu	Thr	Glu	Gln	Leu	Ser	Glu	Glu	Glu	Glu	220
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	225
Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Ser	Gly	Asn	Gln	Ser	Asp	Arg	230
Ser	Gly	Ser	Ser	Gly	Arg	Arg	Lys	Ala	Lys	Lys	Lys	Trp	Arg	Lys	235
Asp	Ser	Pro	Trp	Val	Lys	Pro	Ser	Arg	Lys	Arg	Arg	Lys	Arg	Glu	240
Pro	Pro	Arg	Ala	Lys	Glu	Pro	Arg	Gly	Val	Ser	Asn	Asp	Thr	Ser	245
Ser	Leu	Glu	Thr	Glu	Arg	Gly	Phe	Glu	Glu	Leu	Pro	Leu	Cys	Ser	250
Cys	Arg	Met	Glu	Ala	Pro	Lys	Ile	Asp	Arg	Ile	Ser	Glu	Arg	Ala	255
Gly	His	Lys	Cys	Met	Ala	Thr	Glu	Ser	Val	Asp	Gly	Glu	Leu	Ser	260
Gly	Cys	Asn	Ala	Ala	Ile	Leu	Lys	Arg	Glu	Thr	Met	Arg	Pro	Ser	265
Ser	Arg	Val	Ala	Leu	Met	Val	Leu	Cys	Glu	Thr	His	Arg	Ala	Arg	270
Met	Val	Lys	His	His	Cys	Cys	Pro	Gly	Cys	Gly	Tyr	Phe	Cys	Thr	275
Ala	Gly	Thr	Phe	Leu	Glu	Cys	His	Pro	Asp	Phe	Arg	Val	Ala	His	280
Arg	Phe	His	Lys	Ala	Cys	Val	Ser	Gln	Leu	Asn	Gly	Met	Val	Phe	285
Cys	Pro	His	Cys	Gly	Glu	Asp	Ala	Ser	Glu	Ala	Gln	Glu	Val	Thr	290
Ile	Pro	Arg	Gly	Asp	Gly	Val	Thr	Pro	Pro	Ala	Gly	Thr	Ala	Ala	295
Pro	Ala	Pro	Pro	Pro	Leu	Ser	Gln	Asp	Val	Pro	Gly	Arg	Ala	Asp	300
Thr	Ser	Gln	Pro	Ser	Ala	Arg	Met	Arg	Gly	His	Gly	Glu	Pro	Arg	305
Arg	Pro	Pro	Cys	Asp	Pro	Leu	Ala	Asp	Thr	Ile	Asp	Ser	Ser	Gly	310
Pro	Ser	Leu	Thr	Leu	Pro	Asn	Gly	Gly	Cys	Leu	Ser	Ala	Val	Gly	315
Leu	Pro	Leu	Gly	Pro	Gly	Arg	Glu	Ala	Leu	Glu	Lys	Ala	Leu	Val	320
Ile	Gln	Glu	Ser	Glu	Arg	Arg	Lys	Lys	Leu	Arg	Phe	His	Pro	Arg	325
Gln	Leu	Tyr	Leu	Ser	Val	Lys	Gln	Gly	Glu	Leu	Gln	Lys	Val	Ile	330
Leu	Met	Leu	Leu	Asp	Asn	Leu	Asp	Pro	Asn	Phe	Gln	Ser	Asp	Gln	335



Gln Ser Lys Arg	Thr Pro Leu His Ala	Ala Ala Gln Lys Gly	Ser
635	640	645	
Val Glu Ile Cys	His Val Leu Leu Gln	Ala Gly Ala Asn Ile	Asn
650	655	660	
Ala Val Asp Lys	Gln Gln Arg Thr Pro	Leu Met Glu Ala Val	Val
665	670	675	
Asn Asn His Leu	Glu Val Ala Arg Tyr	Met Val Gln Arg Gly	Gly
680	685	690	
Cys Val Tyr Ser	Lys Glu Glu Asp Gly	Ser Thr Cys Leu His	His
695	700	705	
Ala Ala Lys Ile	Gly Asn Leu Glu Met	Val Ser Leu Leu Leu	Ser
710	715	720	
Thr Gly Gln Val	Asp Val Asn Ala Gln	Asp Ser Gly Gly Trp	Thr
725	730	735	
Pro Ile Ile Trp	Ala Ala Glu His Lys	His Ile Glu Val Ile	Arg
740	745	750	
Met Leu Leu Thr	Arg Gly Ala Asp Val	Thr Leu Thr Asp Asn	Val
755	760	765	
Ser Glu Arg Leu	Val Glu Val Gly Gln	Pro Gln Ala Pro Glu	Gln
770	775	780	
Gly Gly Gly Trp	Ile Gln Gly Pro Ser	Cys Cys Thr Ser Ser	Val
785	790	795	
Pro Leu Leu Pro	Pro Gln Glu Glu Asn	Ile Cys Leu His Trp	Ala
800	805	810	
Ser Phe Thr Gly	Ser Ala Ala Ile Ala	Glu Val Leu	
815	820	825	
830	835		

&lt;210&gt; 193

&lt;211&gt; 445

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:899263.10.orf2:2002JAN18

&lt;400&gt; 193

Leu Lys His Gly Ile	Ser Asp Val Thr Cys	Pro Lys Trp His	Ser
1	5	10	15
Arg Leu Ile Asn Gly	Leu Gly Cys Lys Leu	Ser Phe Ile Pro	Trp
20	25	30	
Asp Ala Leu Ser Ala	Leu Gln His Leu Lys	Phe Arg Gln Arg	Glu
35	40	45	
Leu Thr Trp Gly Gln	Ala Ala Pro Leu Gly	Arg Val Glu Asp	Arg
50	55	60	
Val Ser Leu Leu Ile	Phe Arg Lys Ser Ser	Arg Thr Gln Ser	Pro
65	70	75	
Ala Phe Gly Ser Leu	Ser Gln Arg Asp Arg	Arg Asn Pro Glu	Gln
80	85	90	
Ala Thr Gly Arg Arg	Ser Gly Met Tyr Phe	Cys Trp Gly Ala	Asp
95	100	105	
Ser Arg Glu Leu Gln	Arg Arg Arg Thr Ala	Gly Ser Pro Gly	Ala
110	115	120	
Glu Leu Leu Gln Ala	Ala Ser Gly Glu Arg	His Ser Leu Leu	Leu
125	130	135	
Leu Thr Asn His Arg	Val Leu Ser Cys Gly	Asp Asn Ser Arg	Gly
140	145	150	
Gln Leu Gly Arg Arg	Gly Ala Gln Arg Gly	Glu Leu Pro Glu	Pro
155	160	165	
Ile Gln Ala Leu Glu	Thr Leu Ile Val Asp	Leu Val Ser Cys	Gly
170	175	180	
Lys Glu His Ser Leu	Ala Val Cys His Lys	Gly Arg Val Phe	Ala

Trp Gly Ala Gly	185	190	195
Ser Glu Gly Gln Leu	200	Gly Ile Gly Glu Phe	Lys
Glu Ile Ser Phe Thr	215	Met Thr Leu Asn Asp	Ile
Lys Ile Ile Gln Val	230	Tyr His Ser Leu Ala	Leu
Ser Lys Asp Ser Gln	245	Gly Lys Asn Ser His	Gly
Gln Leu Gly Leu Gly	260	Lys Glu Phe Pro Ser	Gln Ala Ser Pro Gln
Arg Val Arg Ser Leu	275	Glu Gly Ile Pro Leu	Ala Gln Val Ala Ala
Gly Gly Ala His Ser	290	Phe Ala Leu Ser Leu	Cys Gly Thr Ser Phe
Gly Trp Gly Ser Asn	305	Ser Ala Gly Gln Leu	Ala Leu Ser Gly Arg
Asn Val Pro Val Gln	320	Ser Asn Lys Pro Leu	Ser Val Gly Ala Leu
Lys Asn Leu Gly Val	335	Tyr Ile Ser Cys Gly	Asp Ala His Thr
Ala Val Leu Thr Gln	350	Asp Gly Lys Val Phe	Thr Phe Gly Asp Asn
Arg Ser Gly Gln Leu	365	Gly Tyr Ser Pro Thr	Pro Glu Lys Arg Gly
Pro Gln Leu Val Glu	380	Arg Ile Asp Gly Leu	Val Ser Gln Ile Asp
Cys Gly Ser Tyr His	395	Thr Leu Ala Tyr Val	His Thr Thr Gly Gln
Val Val Ser Phe Gly	410	His Gly Pro Ser Asp	Thr Ser Lys Pro Thr
His Pro Glu Ala Leu	425	Thr Glu Asn Phe Asp	Ile Ser Cys Leu Ile
Ser Ala Glu Glu Thr	440	Leu Ser Met Asp Leu	

&lt;210&gt; 194

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:977837.31.orf1:2002JAN18

&lt;400&gt; 194

Phe Thr Cys Arg Asn	1	5	10	15
Ile Thr Leu Leu Arg	20	25	30	35
Cys Gln Leu Lys Trp	40	45	50	55
Gln Ser Phe Val Asn	60	65	70	75
Gly Arg Ser Ile Phe	80	85	90	95
Asp Phe Pro Lys Pro	100	105	110	115
Ala Ile Lys Gly Ser	120	125	130	135
Ser Ser Asp Ser Pro	140	145	150	155
Tyr Cys Met Met Leu	160	165	170	175
Lys Trp Lys Ile Met	180	185	190	195

Lys Val Ala Arg 125 130 135

<210> 195

<211> 650

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Incyte ID No: LG:978560.13.orf2:2002JAN18

<400> 195

Leu	Pro	Phe	Ser	Glu	Asp	Gly	Ser	Ser	Val	Pro	His	Ile	Cys	His
1				5					10					15
Val	His	Pro	Gly	Phe	His	Leu	Ser	Pro	Gly	Leu	Arg	Ile	Ser	Cys
				20					25					30
Phe	Phe	Lys	Arg	Pro	Phe	Leu	Ser	Pro	Glu	Phe	Gly	Pro	Val	Arg
				35					40					45
Val	Gln	Trp	Ser	Gly	Ala	Ser	His	Thr	Gln	Cys	Trp	Phe	Pro	Gly
				50					55					60
Ile	Gly	Asp	Phe	Pro	Arg	Cys	Arg	Cys	Gly	Leu	Tyr	Arg	Glu	Gly
				65					70					75
Val	Ala	Leu	Ala	Gly	Phe	Phe	Ser	Glu	Lys	Thr	Val	Gln	Arg	Cys
				80					85					90
Asn	Ala	Gly	Glu	Leu	Gln	Gln	Pro	His	Phe	Thr	Gly	Asn	Phe	Gly
				95					100					105
Thr	Thr	His	Phe	Ala	Ala	Pro	Lys	Ser	Asp	Leu	Ser	Thr	Leu	Arg
				110					115					120
Ser	Ile	Glu	Asp	Pro	Ser	Val	Glu	Pro	Arg	Leu	Leu	Glu	Gly	Val
				125					130					135
Val	Pro	Leu	His	Gly	Pro	Pro	Ser	Thr	Cys	Val	Phe	Pro	Val	Ser
				140					145					150
Val	Gly	Tyr	Gln	Val	Gly	Lys	Pro	Ser	Leu	Ile	Ser	His	Leu	Glu
				155					160					165
Gln	Glu	Glu	Glu	Pro	Arg	Thr	Glu	Glu	Arg	Gly	Ala	His	Gln	Gly
				170					175					180
Ala	Cys	Ala	Asp	Trp	Glu	Thr	Pro	Ser	Lys	Thr	Lys	Trp	Ser	Leu
				185					190					195
Leu	Met	Glu	Asp	Ile	Phe	Gly	Lys	Glu	Thr	Pro	Ser	Gly	Val	Thr
				200					205					210
Met	Glu	Arg	Ala	Gly	Leu	Gly	Glu	Lys	Ser	Thr	Glu	Tyr	Ala	His
				215					220					225
Leu	Phe	Glu	Val	Phe	Gly	Met	Asp	Pro	His	Leu	Thr	Gln	Pro	Met
				230					235					240
Gly	Arg	His	Ala	Gly	Lys	Arg	Pro	Tyr	His	Arg	Arg	Asp	Tyr	Gly
				245					250					255
Val	Ala	Phe	Lys	Gly	Arg	Pro	His	Leu	Thr	Gln	His	Met	Ser	Met
				260					265					270
Tyr	Asp	Gly	Arg	Lys	Met	His	Glu	Cys	His	Gln	Cys	Gln	Lys	Ala
				275					280					285
Phe	Thr	Thr	Ser	Ala	Ser	Leu	Thr	Arg	His	Arg	Arg	Ile	His	Thr
				290					295					300
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Ser	Asp	Cys	Gly	Lys	Ala	Phe	Asn
				305					310					315
Asp	Pro	Ser	Ala	Leu	Arg	Ser	His	Ala	Arg	Thr	His	Leu	Lys	Glu
				320					325					330
Lys	Pro	Phe	Asp	Cys	Ser	Gln	Cys	Gly	Asn	Ala	Phe	Arg	Thr	Leu
				335					340					345
Ser	Ala	Leu	Lys	Ile	His	Met	Arg	Val	His	Thr	Gly	Glu	Arg	Pro
				350					355					360
Tyr	Lys	Cys	Asp	Gln	Cys	Gly	Lys	Ala	Tyr	Gly	Arg	Ser	Cys	His

	365		370		375
Leu Ile Ala His	Lys Arg Thr His Thr	Gly Glu Arg Pro Tyr	Glu		
	380		385		390
Cys His Asp Cys	Gly Lys Ala Phe Gln	His Pro Ser His Leu	Lys		
	395		400		405
Glu His Val Arg	Asn His Thr Gly Glu	Lys Pro Tyr Ala Cys	Thr		
	410		415		420
Gln Cys Gly Lys	Ala Phe Arg Trp Lys	Ser Asn Phe Asn Leu	His		
	425		430		435
Lys Lys Asn His	Met Val Glu Lys Thr	Tyr Glu Cys Lys Glu	Cys		
	440		445		450
Gly Lys Ser Phe	Gly Asp Leu Val Ser	Arg Arg Lys His Met	Arg		
	455		460		465
Ile His Ile Val	Lys Lys Pro Val Glu	Cys Arg Gln Cys Gly	Lys		
	470		475		480
Thr Phe Arg Asn	Gln Ser Ile Leu Lys	Thr His Met Asn Ser	His		
	485		490		495
Thr Gly Glu Lys	Pro Tyr Gly Cys Asp	Leu Cys Gly Lys Ala	Phe		
	500		505		510
Ser Ala Ser Ser	Asn Leu Thr Ala His	Arg Lys Ile His Thr	Gln		
	515		520		525
Glu Arg Arg Tyr	Glu Cys Ala Ala Cys	Gly Lys Val Phe Gly	Asp		
	530		535		540
Tyr Leu Ser Arg	Arg Arg His Met Ser	Val His Leu Val Lys	Lys		
	545		550		555
Arg Val Glu Cys	Arg Gln Cys Gly Lys	Ala Phe Arg Asn Gln	Ser		
	560		565		570
Thr Leu Lys Thr	His Met Arg Ser His	Thr Gly Glu Lys Pro	Tyr		
	575		580		585
Glu Cys Asp His	Cys Gly Lys Ala Phe	Ser Ile Gly Ser Asn	Leu		
	590		595		600
Asn Val His Arg	Arg Ile His Thr Gly	Glu Lys Pro Tyr Glu	Cys		
	605		610		615
Leu Val Cys Gly	Lys Ala Phe Ser Asp	His Ser Ser Leu Arg	Ser		
	620		625		630
His Val Lys Thr	His Arg Gly Glu Lys	Leu Phe Val Ser Ser	Val		
	635		640		645
Trp Lys Arg Leu	Gln				
	650				

&lt;210&gt; 196

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:979390.2.orf1:2002JAN18

&lt;400&gt; 196

Asn Ser Leu Ser Val	Ala Ser Ala Pro Pro	Gln Arg Asp Pro Gly
1	5	10
Met Ala Met Ala Leu	Pro Met Pro Gly Pro	Gln Glu Ala Val Val
	20	25
Phe Glu Asp Val Ala	Val Tyr Phe Thr Arg	Ile Glu Trp Ser Cys
	35	40
Leu Ala Pro Asp Gln	Gln Ala Leu Tyr Arg	Asp Val Met Leu Glu
	50	55
Asn Tyr Gly Asn Leu	Ala Ser Leu Gly Phe	Leu Val Ala Lys Pro
	65	70
Ala Leu Ile Ser Leu	Leu Glu Gln Gly Glu	Glu Pro Gly Ala Leu
	80	85
Ile Leu Gln Val Ala	Glu Gln Ser Val Ala	Lys Ala Ser Leu Cys

	95		100		105
Thr Glu Asp Pro Asn	Thr Leu Pro Ser Arg	Ser Gln Glu Gly Ser			
110	115	120			
Pro Ala Ser Ser Glu	Gly Gly Pro Gly Glu	Lys Gly Val Ala Gly			
125	130	135			
Arg Val Ala Gly Gly	Gly Ala Ala Ser Ser	Trp Pro His Gly Glu			
140	145	150			
His Pro Val Thr Pro	Asn Arg				
155					

&lt;210&gt; 197

&lt;211&gt; 431

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:983019.1.orf2:2002JAN18

&lt;400&gt; 197

Arg Leu Trp Leu Lys	Phe His Arg His Gln	Thr Glu Met Ile Ile
1	5	10
Thr Lys Gln Gly Arg	Arg Met Phe Pro Phe	Leu Ser Phe Asn Ile
20	25	30
Asn Gly Leu Asn Pro	Thr Ala His Tyr Asn	Val Phe Val Glu Val
35	40	45
Val Leu Ala Asp Pro	Asn His Trp Arg Phe	Gln Gly Gly Lys Trp
50	55	60
Val Thr Cys Gly Lys	Ala Asp Asn Asn Met	Gln Gly Asn Lys Met
65	70	75
Tyr Val His Pro Glu	Ser Pro Asn Thr Gly	Ser His Trp Met Arg
80	85	90
Gln Glu Ile Ser Phe	Gly Lys Leu Lys Leu	Thr Asn Asn Lys Gly
95	100	105
Ala Asn Asn Asn Asn	Thr Gln Met Ile Val	Leu Gln Ser Leu His
110	115	120
Lys Tyr Gln Pro Arg	Leu His Ile Val Glu	Val Thr Glu Asp Gly
125	130	135
Val Glu Asp Leu Asn	Glu Pro Ser Lys Thr	Gln Thr Phe Thr Phe
140	145	150
Ser Glu Thr Gln Phe	Ile Ala Val Thr Ala	Tyr Gln Asn Thr Asp
155	160	165
Ile Thr Gln Leu Lys	Ile Asp His Asn Pro	Phe Ala Lys Gly Phe
170	175	180
Arg Asp Asn Tyr Asp	Ser Met Tyr Thr Ala	Ser Glu Asn Asp Arg
185	190	195
Leu Thr Pro Ser Pro	Thr Asp Ser Pro Arg	Ser His Gln Ile Val
200	205	210
Pro Gly Gly Arg Tyr	Gly Val Gln Ser Phe	Phe Pro Glu Pro Phe
215	220	225
Val Asn Thr Leu Pro	Gln Ala Arg Tyr Tyr	Asn Gly Glu Arg Thr
230	235	240
Val Pro Gln Thr Asn	Gly Leu Leu Ser Pro	Gln Gln Ser Glu Glu
245	250	255
Val Ala Asn Pro Pro	Gln Arg Trp Leu Val	Thr Pro Val Gln Gln
260	265	270
Pro Gly Thr Asn Lys	Leu Asp Ile Ser Ser	Tyr Glu Ser Glu Tyr
275	280	285
Thr Ser Ser Thr Leu	Leu Pro Tyr Gly Ile	Lys Ser Leu Pro Leu
290	295	300
Gln Thr Ser His Ala	Leu Gly Tyr Tyr Pro	Asp Pro Thr Phe Pro
305	310	315
Ala Met Ala Gly Trp	Gly Gly Arg Gly Ser	Tyr Gln Arg Lys Met

Ala	Ala	Gly	Leu	320	Pro	Trp	Thr	Ser	Arg	Thr	Ser	Pro	Thr	Val	Phe	330
				335												345
Ser	Glu	Asp	Gln	350	Leu	Ser	Lys	Glu	Lys	Val	Lys	Glu	Glu	Ile	Gly	360
Ser	Ser	Trp	Ile	365	Glu	Thr	Pro	Pro	Ser	Ile	Lys	Ser	Leu	Asp	Ser	375
Asn	Asp	Ser	Gly	380	Val	Tyr	Thr	Ser	Ala	Cys	Lys	Arg	Arg	Arg	Leu	390
Ser	Pro	Ser	Asn	395	Ser	Ser	Asn	Glu	Asn	Ser	Pro	Ser	Ile	Lys	Cys	405
Glu	Asp	Ile	Asn	410	Ala	Glu	Glu	Tyr	Ser	Lys	Asp	Thr	Ser	Lys	Gly	420
Met	Gly	Gly	Tyr	425	Ala	Phe	Tyr	Thr	Thr	Pro						430

&lt;210&gt; 198

&lt;211&gt; 975

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:997202.7.orf2:2002JAN18

&lt;400&gt; 198

Ser	Leu	Ser	Gly	Phe	Thr	Arg	Glu	Ala	Ser	Phe	Glu	Met	Ala	Ala		
1				5					10					15		
Gln	Arg	Ile	Arg	Ala	Ala	Asn	Ser	Asn	Gly	Leu	Pro	Arg	Cys	Lys		
				20					25					30		
Ser	Glu	Gly	Thr	Leu	Ile	Asp	Leu	Ser	Glu	Gly	Phe	Ser	Glu	Thr		
				35					40					45		
Ser	Phe	Asn	Asp	Ile	Lys	Val	Pro	Ser	Pro	Ser	Ala	Leu	Leu	Val		
				50					55					60		
Asp	Asn	Pro	Thr	Pro	Phe	Gly	Asn	Ala	Lys	Glu	Val	Ile	Ala	Ile		
				65					70					75		
Lys	Asp	Tyr	Cys	Pro	Thr	Asn	Phe	Thr	Thr	Leu	Lys	Phe	Ser	Lys		
				80					85					90		
Gly	Asp	His	Leu	Tyr	Val	Leu	Asp	Thr	Ser	Gly	Gly	Glu	Trp	Trp		
				95					100					105		
Tyr	Ala	His	Asn	Thr	Thr	Glu	Met	Gly	Tyr	Ile	Pro	Ser	Ser	Tyr		
				110					115					120		
Val	Gln	Pro	Leu	Asn	Tyr	Arg	Asn	Ser	Thr	Leu	Ser	Asp	Ser	Gly		
				125					130					135		
Met	Ile	Asp	Asn	Leu	Pro	Asp	Ser	Pro	Asp	Glu	Val	Ala	Lys	Glu		
				140					145					150		
Leu	Glu	Leu	Leu	Gly	Gly	Trp	Thr	Asp	Asp	Lys	Lys	Val	Pro	Gly		
				155					160					165		
Arg	Met	Tyr	Ser	Asn	Asn	Pro	Phe	Trp	Asn	Gly	Val	Gln	Thr	Asn		
				170					175					180		
Pro	Phe	Leu	Asn	Gly	Asn	Val	Pro	Val	Met	Pro	Ser	Leu	Asp	Glu		
				185					190					195		
Leu	Asn	Pro	Lys	Ser	Thr	Val	Asp	Leu	Leu	Leu	Phe	Asp	Ala	Gly		
				200					205					210		
Thr	Ser	Ser	Phe	Thr	Glu	Ser	Ser	Ser	Ala	Thr	Thr	Asn	Ser	Thr		
				215					220					225		
Gly	Asn	Ile	Phe	Asp	Glu	Leu	Pro	Val	Thr	Asn	Gly	Leu	His	Ala		
				230					235					240		
Glu	Pro	Pro	Val	Arg	Arg	Asp	Asn	Pro	Phe	Phe	Arg	Ser	Lys	Arg		
				245					250					255		
Ser	Tyr	Ser	Leu	Ser	Glu	Leu	Ser	Val	Leu	Gln	Ala	Lys	Ser	Asp		
				260					265					270		
Ala	Pro	Thr	Ser	Ser	Ser	Phe	Phe	Thr	Gly	Leu	Lys	Ser	Pro	Ala		

	275		280	285
Pro Glu Gln Phe	Gln Ser Arg Glu Asp	Phe Arg Thr Ala Trp	Leu	
	290		295	300
Asn His Arg Lys	Leu Ala Arg Ser Cys	His Asp Leu Asp Leu	Leu	
	305		310	315
Gly Gln Ser Pro	Gly Trp Gly Gln Thr	Gln Ala Val Glu Thr	Asn	
	320		325	330
Ile Val Cys Lys	Leu Asp Ser Ser Gly	Gly Ala Val Gln Leu	Pro	
	335		340	345
Asp Thr Ser Ile	Ser Ile His Val Pro	Glu Gly His Val Ala	Pro	
	350		355	360
Gly Glu Thr Gln	Gln Ile Ser Met Lys	Ala Leu Leu Asp Pro	Pro	
	365		370	375
Leu Glu Leu Asn	Ser Asp Arg Ser Cys	Ser Ile Ser Pro Val	Leu	
	380		385	390
Glu Val Lys Leu	Ser Asn Leu Glu Val	Lys Thr Ser Ile Ile	Leu	
	395		400	405
Glu Met Lys Val	Ser Ala Glu Ile Lys	Asn Asp Leu Phe Ser	Lys	
	410		415	420
Ser Thr Val Gly	Leu Gln Cys Leu Arg	Ser Asp Ser Lys Glu	Gly	
	425		430	435
Pro Tyr Val Ser	Val Pro Leu Asn Cys	Ser Cys Gly Asp Thr	Val	
	440		445	450
Gln Ala Gln Leu	His Asn Leu Glu Pro	Cys Met Tyr Val Ala	Val	
	455		460	465
Val Ala His Gly	Pro Ser Ile Leu Tyr	Pro Ser Thr Val Trp	Asp	
	470		475	480
Phe Ile Asn Lys	Lys Val Thr Val Gly	Leu Tyr Gly Pro Lys	His	
	485		490	495
Ile His Pro Ser	Phe Lys Thr Val Val	Thr Ile Phe Gly His	Asp	
	500		505	510
Cys Ala Pro Lys	Thr Leu Leu Val Ser	Glu Val Thr Arg Gln	Ala	
	515		520	525
Pro Asn Pro Ala	Pro Val Ala Leu Gln	Leu Trp Gly Lys His	Gln	
	530		535	540
Phe Val Leu Ser	Arg Pro Gln Asp Leu	Lys Val Cys Met Phe	Ser	
	545		550	555
Asn Met Thr Asn	Tyr Glu Val Lys Ala	Ser Glu Gln Ala Lys	Val	
	560		565	570
Val Arg Gly Phe	Gln Leu Lys Leu Gly	Lys Val Ser Arg Leu	Ile	
	575		580	585
Phe Pro Ile Thr	Ser Gln Asn Pro Asn	Glu Leu Ser Asp Phe	Thr	
	590		595	600
Leu Arg Val Gln	Val Lys Asp Asp Gln	Glu Ala Ile Leu Thr	Gln	
	605		610	615
Phe Cys Val Gln	Thr Pro Gln Pro Pro	Pro Lys Ser Ala Ile	Lys	
	620		625	630
Pro Ser Gly Gln	Arg Arg Phe Leu Lys	Lys Asn Glu Val Gly	Lys	
	635		640	645
Ile Ile Leu Ser	Pro Phe Ala Thr Thr	Thr Lys Tyr Pro Thr	Phe	
	650		655	660
Gln Asp Arg Pro	Val Ser Ser Leu Lys	Phe Gly Lys Leu Leu	Lys	
	665		670	675
Thr Val Val Arg	Gln Asn Lys Asn His	Tyr Leu Leu Glu Tyr	Lys	
	680		685	690
Lys Gly Asp Gly	Ile Ala Leu Leu Ser	Glu Glu Arg Val Arg	Leu	
	695		700	705
Arg Gly Gln Leu	Trp Thr Lys Glu Trp	Tyr Ile Gly Tyr Tyr	Gln	
	710		715	720
Gly Arg Val Gly	Leu Val His Thr Lys	Asn Val Leu Val Val	Gly	
	725		730	735
Arg Ala Arg Pro	Ser Leu Cys Ser Gly	Pro Glu Leu Ser Thr	Ser	
	740		745	750

Val	Leu	Leu	Glu	Gln	Ile	Leu	Arg	Pro	Cys	Lys	Phe	Leu	Thr	Tyr	
				755					760					765	
Ile	Tyr	Ala	Ser	Val	Arg	Thr	Leu	Leu	Met	Glu	Asn	Ile	Ser	Ser	
				770					775					780	
Trp	Arg	Ser	Phe	Ala	Asp	Ala	Leu	Gly	Tyr	Val	Asn	Leu	Pro	Leu	
				785					790					795	
Thr	Phe	Phe	Cys	Arg	Ala	Glu	Leu	Asp	Ser	Glu	Pro	Glu	Arg	Val	
				800					805					810	
Ala	Ser	Val	Leu	Glu	Lys	Leu	Lys	Glu	Asp	Cys	Asn	Asn	Thr	Glu	
				815					820					825	
Asn	Lys	Glu	Arg	Lys	Ser	Phe	Gln	Lys	Glu	Leu	Val	Met	Ala	Leu	
				830					835					840	
Leu	Lys	Met	Asp	Cys	Gln	Gly	Leu	Val	Val	Arg	Leu	Ile	Gln	Asp	
				845					850					855	
Phe	Val	Leu	Leu	Thr	Thr	Ala	Val	Glu	Val	Ala	Gln	Arg	Trp	Arg	
				860					865					870	
Glu	Leu	Ala	Glu	Lys	Leu	Ala	Lys	Val	Ser	Lys	Gln	Gln	Met	Asp	
				875					880					885	
Ala	Tyr	Glu	Ser	Pro	His	Arg	Asp	Arg	Asn	Gly	Val	Val	Asp	Ser	
				890					895					900	
Glu	Ala	Met	Trp	Lys	Pro	Ala	Tyr	Asp	Phe	Leu	Leu	Thr	Trp	Ser	
				905					910					915	
His	Gln	Ile	Gly	Asp	Ser	Tyr	Arg	Asp	Val	Ile	Gln	Glu	Leu	His	
				920					925					930	
Leu	Gly	Leu	Asp	Lys	Met	Lys	Asn	Pro	Ile	Thr	Lys	Arg	Trp	Lys	
				935					940					945	
His	Leu	Thr	Gly	Thr	Leu	Ile	Leu	Val	Asn	Ser	Leu	Asp	Val	Leu	
				950					955					960	
Arg	Ala	Ala	Ala	Phe	Ser	Pro	Ala	Asp	Gln	Asp	Asp	Phe	Val	Ile	
				965					970					975	

&lt;210&gt; 199

&lt;211&gt; 484

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:998756.3.orf1:2002JAN18

&lt;400&gt; 199

Gly	Gly	Gly	Pro	Met	Lys	Asp	Cys	Glu	Tyr	Ser	Gln	Ile	Ser	Thr	
1				5					10					15	
His	Ser	Ser	Ser	Pro	Met	Glu	Ser	Pro	His	Lys	Lys	Lys	Lys	Ile	
				20					25					30	
Ala	Ala	Arg	Arg	Lys	Trp	Glu	Val	Phe	Pro	Gly	Arg	Asn	Lys	Phe	
				35					40					45	
Phe	Cys	Asn	Gly	Arg	Ile	Met	Met	Ala	Arg	Gln	Thr	Gly	Val	Phe	
				50					55					60	
Tyr	Leu	Thr	Leu	Val	Leu	Ile	Leu	Val	Thr	Ser	Gly	Leu	Phe	Phe	
				65					70					75	
Ala	Phe	Asp	Cys	Pro	Tyr	Leu	Ala	Val	Lys	Ile	Thr	Pro	Ala	Ile	
				80					85					90	
Pro	Ala	Val	Ala	Gly	Ile	Leu	Phe	Phe	Phe	Val	Met	Gly	Thr	Leu	
				95					100					105	
Leu	Arg	Thr	Ser	Phe	Ser	Asp	Pro	Gly	Val	Leu	Pro	Arg	Ala	Thr	
				110					115					120	
Pro	Asp	Glu	Ala	Ala	Asp	Leu	Glu	Arg	Gln	Ile	Asp	Ile	Ala	Asn	
				125					130					135	
Gly	Thr	Ser	Ser	Gly	Gly	Tyr	Arg	Pro	Pro	Pro	Arg	Thr	Lys	Glu	
				140					145					150	
Val	Ile	Ile	Asn	Gly	Gln	Thr	Val	Lys	Leu	Lys	Tyr	Cys	Phe	Thr	



Cys Lys Ile Phe	Arg Pro Pro Arg Ala	Ser His Cys Ser Leu	Cys
Asp Asn Cys Val	Glu Arg Phe Asp His	His Cys Pro Trp Val	Gly
Asn Cys Val Gly	Lys Arg Asn Tyr Arg	Phe Phe Tyr Met Phe	Ile
Leu Ser Leu Ser	Phe Leu Thr Val Phe	Ile Phe Ala Phe Val	Ile
Thr His Val Ile	Leu Arg Ser Gln Gln	Thr Gly Phe Leu Asn	Ala
Leu Lys Asp Ser	Pro Ala Ser Val Leu	Glu Ala Val Val Cys	Phe
Phe Ser Val Trp	Ser Ile Val Gly Leu	Ser Gly Phe His Thr	Tyr
Leu Ile Ser Ser	Asn Gln Thr Thr Asn	Glu Asp Ile Lys Gly	Ser
Trp Ser Asn Lys	Arg Gly Lys Glu Asn	Tyr Asn Pro Tyr Ser	Tyr
Gly Asn Ile Phe	Thr Asn Cys Cys Val	Ala Leu Cys Gly Pro	Ile
Ser Pro Ser Leu	Ile Asp Arg Arg Gly	Tyr Ile Gln Pro Asp	Thr
Pro Gln Pro Ala	Ala Pro Ser Asn Gly	Ile Thr Met Tyr Gly	Ala
Thr Gln Ser Gln	Ser Asp Met Cys Asp	Gln Asp Gln Cys Ile	Gln
Ser Thr Lys Phe	Val Leu Gln Ala Ala	Ala Thr Pro Leu Leu	Gln
Ser Glu Pro Ser	Leu Thr Ser Asp Glu	Leu His Leu Pro Gly	Lys
Pro Gly Leu Gly	Thr Pro Cys Ala Ser	Leu Thr Leu Gly Pro	Pro
Thr Pro Pro Ala	Ser Met Pro Asn Leu	Ala Glu Ala Thr Leu	Ala
Asp Val Met Pro	Arg Lys Asp Glu His	Met Gly His Gln Phe	Leu
Thr Pro Asp Glu	Ala Pro Ser Pro Pro	Arg Leu Leu Ala Ala	Gly
Ser Pro Leu Ala	His Ser Arg Thr Met	His Val Leu Gly Leu	Ala
Ser Gln Asp Ser	Leu His Glu Asp Ser	Val Arg Gly Leu Val	Lys
Leu Ser Ser Val			

&lt;210&gt; 200

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:103460.28.orf2:2002JAN18

&lt;400&gt; 200

Gln Arg His Gly His	Met Pro Gln Ala Phe	Leu Leu Gly Ser Ile
1	5	10
His Glu Pro Ala Gly	Ala Leu Met Glu Pro	Gln Pro Cys Pro Gly
20	25	30
Ser Leu Ala Glu Ser	Phe Leu Glu Glu Leu	Arg Leu Asn Ala
35	40	45
Glu Leu Ser Gln Leu	Gln Phe Ser Glu Pro	Val Gly Ile Ile Tyr

50	55	60
Asn Pro Val Glu Tyr Ala Trp Glu Pro His Arg Asn Tyr Val Thr		
65	70	75
Arg Tyr Cys Gln Gly Pro Lys Glu Val Leu Phe Leu Gly Met Asn		
80	85	90
Pro Gly Pro Phe Gly Met Ala Gln Thr Gly Val Pro Phe Gly Glu		
95	100	105
Val Ser Met Val Arg Asp Trp Leu Gly Ile Val Gly Pro Val Leu		
110	115	120
Thr Pro Pro Gln Glu His Pro Lys Arg Pro Val Leu Gly Leu Glu		
125	130	135
Cys Pro Gln Ser Glu Val Ser Gly Ala Arg Phe Trp Gly Phe Phe		
140	145	150
Arg Asn Leu Cys Gly Gln Pro Glu Val Phe Phe His His Cys Phe		
155	160	165
Val His Asn Leu Cys Pro Leu Leu Phe Leu Ala Pro Ser Gly Arg		
170	175	180
Asn Leu Thr Pro Ala Glu Leu Pro Ala Lys Gln Arg Glu Gln Leu		
185	190	195
Leu Gly Ile Cys Asp Ala Ala Leu Cys Arg Gln Val Gln Leu Leu		
200	205	210
Gly Val Arg Leu Val Val Gly Val Gly Arg Leu Ala Glu Gln Arg		
215	220	225
Ala Arg Arg Ala Leu Ala Gly Leu Met Pro Glu Val Gln Val Glu		
230	235	240
Gly Leu Leu His Pro Ser Pro Arg Asn Pro Gln Ala Asn Lys Gly		
245	250	255
Trp Glu Ala Val Ala Lys Glu Arg Leu Asn Glu Leu Gly Leu Leu		
260	265	270
Pro Leu Leu Leu Lys		
275		

&lt;210&gt; 201

&lt;211&gt; 245

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:1501505.19.orf1:2002JAN18

&lt;400&gt; 201

Lys Ala Phe Ala Ser Gln Asn Asn Tyr Arg Ile Asp Ala Asn Gln	
1 5 10 15	
Glu Leu Leu Ala Ile Gly Leu Thr Asn Met Leu Gly Ser Leu Val	
20 25 30	
Ser Ser Tyr Pro Val Thr Gly Ser Phe Gly Arg Thr Ala Val Asn	
35 40 45	
Ala Gln Ser Gly Val Cys Thr Pro Ala Gly Gly Leu Val Thr Gly	
50 55 60	
Val Leu Val Leu Leu Ser Leu Asp Tyr Leu Thr Ser Leu Phe Tyr	
65 70 75	
Tyr Ile Pro Lys Ser Ala Leu Ala Ala Val Ile Ile Met Ala Val	
80 85 90	
Ala Pro Leu Phe Asp Thr Lys Ile Phe Arg Thr Leu Trp Arg Val	
95 100 105	
Lys Arg Leu Asp Leu Leu Pro Leu Cys Val Thr Phe Leu Leu Cys	
110 115 120	
Phe Trp Glu Val Gln Tyr Gly Ile Leu Ala Gly Ala Leu Val Ser	
125 130 135	
Leu Leu Met Leu Leu His Ser Ala Ala Arg Pro Glu Thr Lys Val	
140 145 150	
Ser Glu Gly Pro Val Leu Val Leu Gln Pro Ala Ser Gly Leu Ser	

Phe	Pro	Ala	Met	155	Glu	Ala	Leu	Arg	Glu	160	Glu	Ile	Leu	Ser	Arg	Ala	165
				170						175							180
Leu	Glu	Gly	Ala	185	Trp	Ala	Gly	Val	Lys	190	Cys	Pro	Arg	His	Ala	Ala	195
Trp	Ser	Trp	Ser	200	Ala	Pro	Met	Ser	Ala	205	Ala	Ser	Thr	Thr	Leu	Trp	210
Cys	Trp	Asp	Ser	215	Ala	Ser	Ser	Ser	Arg	220	Thr	Ser	Arg	Ser	Arg	Ala	225
Ser	Pro	Trp	Pro	230	Leu	Trp	Ala	Cys	Arg	235	Ser	Pro	Phe	Ser	Val	Ser	240
Cys	Cys	Pro	Leu	245													

&lt;210&gt; 202

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:233444.9.orf2:2002JAN18

&lt;400&gt; 202

Ser	Val	Ser	Cys	Leu	Val	Tyr	Met	Thr	Lys	Gly	Thr	Leu	Ala	Phe			
1				5					10					15			
Ser	Asn	Ala	Trp	20	Thr	Tyr	Leu	Val	Ile	25	Ile	Asn	Asn	Met	Ser	Gln	
Leu	Phe	Ala	Met	35	Tyr	Cys	Leu	Leu	Leu	40	Phe	Tyr	Lys	Val	Leu	Lys	
Glu	Glu	Leu	Ser	50	Pro	Ile	Gln	Pro	Val	55	Gly	Lys	Phe	Leu	Cys	Val	
Lys	Leu	Val	Val	65	Phe	Val	Ser	Phe	Trp	70	Gln	Ala	Val	Val	Ile	Ala	
Leu	Leu	Val	Lys	80	Val	Gly	Val	Ile	Ser	85	Glu	Lys	His	Thr	Trp	Glu	
Trp	Gln	Thr	Val	95	Glu	Ala	Val	Ala	Thr	100	Gly	Leu	Gln	Asp	Phe	Ile	
Ile	Cys	Ile	Glu	110	Met	Phe	Leu	Ala	Ala	115	Ile	Ala	His	His	Tyr	Thr	
Phe	Ser	Tyr	Lys	125	Pro	Tyr	Val	Gln	Glu	130	Ala	Glu	Glu	Gly	Ser	Cys	
Phe	Asp	Ser	Phe	140	Leu	Ala	Met	Trp	Asp	145	Val	Ser	Asp	Ile	Arg	Asp	
Asp	Ile	Ser	Glu	155	Gln	Val	Arg	His	Val	160	Gly	Arg	Thr	Val	Arg	Gly	
His	Pro	Arg	Lys	170	Lys	Leu	Phe	Pro	Glu	175	Asp	Gln	Asp	Gln	Asn	Glu	
His	Thr	Ser	Leu	185	Leu	Ser	Ser	Ser	Ser	190	Gln	Asp	Ala	Ile	Ser	Ile	
Ala	Ser	Ser	Met	200	Pro	Pro	Ser	Pro	Met	205	Gly	His	Tyr	Gln	Gly	Phe	
Gly	His	Thr	Val	215	Thr	Pro	Gln	Thr	Thr	220	Pro	Thr	Thr	Ala	Lys	Ile	
Ser	Asp	Glu	Ile	230	Leu	Ser	Asp	Thr	Ile	235	Gly	Glu	Lys	Lys	Glu	Pro	
Ser	Asp	Lys	Ser	245	Val	Asp	Ser										

&lt;210&gt; 203

&lt;211&gt; 749

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:234824.7.orf2:2002JAN18

&lt;400&gt; 203

Ser	Gln	Pro	Ala	His	Leu	Gly	Ala	Ile	Arg	Leu	Ser	Arg	Ala	Trp
1				5					10					15
Ala	Gly	Phe	Leu	Thr	Leu	Trp	Leu	Asp	Asn	Asn	Arg	Ile	Arg	Tyr
				20					25					30
Leu	Pro	Asp	Ser	Ile	Val	Glu	Leu	Thr	Gly	Leu	Glu	Glu	Leu	Val
				35					40					45
Leu	Gln	Gly	Asn	Gln	Ile	Ala	Val	Leu	Pro	Asp	His	Phe	Gly	Gln
				50					55					60
Leu	Ser	Arg	Val	Gly	Leu	Trp	Lys	Ile	Lys	Asp	Asn	Pro	Leu	Ile
				65					70					75
Gln	Pro	Pro	Tyr	Glu	Val	Cys	Met	Lys	Gly	Ile	Pro	Tyr	Ile	Ala
				80					85					90
Ala	Tyr	Gln	Lys	Glu	Leu	Ala	His	Ser	Gln	Pro	Ala	Val	Gln	Pro
				95					100					105
Arg	Leu	Lys	Leu	Leu	Leu	Met	Gly	His	Lys	Ala	Ala	Gly	Lys	Thr
				110					115					120
Leu	Leu	Arg	His	Cys	Leu	Thr	Glu	Glu	Arg	Val	Glu	Gly	Cys	Pro
				125					130					135
Gly	Gly	Gly	Asp	Lys	Glu	Lys	Cys	Tyr	Pro	Pro	Ser	Pro	Pro	Pro
				140					145					150
Val	Ser	Lys	Gly	Ile	Glu	Val	Thr	Ser	Trp	Thr	Ala	Asp	Ala	Ser
				155					160					165
Arg	Gly	Leu	Arg	Phe	Ile	Val	Tyr	Asp	Leu	Ala	Gly	Asp	Glu	Ser
				170					175					180
Tyr	Glu	Val	Ile	Gln	Pro	Phe	Phe	Leu	Ser	Pro	Gly	Ala	Leu	Tyr
				185					190					195
Val	Leu	Val	Val	Asn	Leu	Ala	Thr	Tyr	Glu	Pro	Arg	His	Phe	Pro
				200					205					210
Thr	Thr	Val	Gly	Ser	Phe	Leu	His	Arg	Val	Gly	Ala	Arg	Val	Pro
				215					220					225
His	Ala	Val	Val	Cys	Ile	Val	Gly	Thr	His	Ala	Asp	Leu	Cys	Gly
				230					235					240
Glu	Arg	Glu	Leu	Glu	Glu	Lys	Cys	Leu	Asp	Ile	His	Arg	Gln	Ile
				245					250					255
Ala	Leu	Gln	Glu	Lys	His	Asp	Ala	Glu	Gly	Leu	Ser	Arg	Leu	Ala
				260					265					270
Lys	Val	Val	Asp	Glu	Ala	Leu	Ala	Arg	Asp	Phe	Glu	Leu	Arg	Ser
				275					280					285
Ala	Ser	Pro	His	Ala	Ala	Tyr	Tyr	Gly	Val	Ser	Asp	Lys	Asn	Leu
				290					295					300
Arg	Arg	Arg	Lys	Ala	His	Phe	Gln	Tyr	Leu	Leu	Asn	His	Arg	Leu
				305					310					315
Gln	Ile	Leu	Ser	Pro	Val	Leu	Pro	Val	Ser	Cys	Arg	Asp	Pro	Arg
				320					325					330
His	Leu	Arg	Arg	Leu	Arg	Asp	Lys	Leu	Leu	Ser	Val	Ala	Glu	His
				335					340					345
Arg	Glu	Ile	Phe	Pro	Asn	Leu	His	Arg	Val	Leu	Pro	Arg	Ser	Trp
				350					355					360
Gln	Val	Leu	Glu	Glu	Leu	His	Phe	Gln	Pro	Pro	Gln	Ala	Gln	Arg
				365					370					375
Leu	Trp	Leu	Ser	Trp	Trp	Asp	Ser	Ala	Arg	Leu	Gly	Leu	Gln	Ala
				380					385					390
Gly	Leu	Thr	Glu	Asp	Arg	Leu	Gln	Ser	Ala	Leu	Ser	Tyr	Leu	His
				395					400					405
Glu	Ser	Gly	Lys	Leu	Leu	Tyr	Phe	Glu	Asp	Ser	Pro	Ala	Leu	Lys
				410					415					420
Glu	His	Val	Phe	His	Asn	Leu	Thr	Arg	Leu	Ile	Asp	Ile	Leu	Asn
				425					430					435

Val	Phe	Phe	Gln	Arg	Asp	Pro	Ser	Leu	Leu	Leu	His	Lys	Leu	Leu			
				440					445								450
Leu	Gly	Thr	Ser	Gly	Glu	Gly	Lys	Ala	Glu	Gly	Glu	Ser	Ser	Pro			
				455					460								465
Pro	Met	Ala	Arg	Ser	Thr	Pro	Ser	Gln	Glu	Leu	Leu	Arg	Ala	Thr			
				470					475								480
Gln	Leu	His	Gln	Tyr	Val	Glu	Gly	Phe	Leu	Leu	His	Gly	Leu	Leu			
				485					490								495
Pro	Ala	His	Val	Ile	Arg	Leu	Leu	Leu	Lys	Pro	His	Val	Gln	Ala			
				500					505								510
Gln	Gln	Asp	Leu	Gln	Leu	Leu	Leu	Glu	Leu	Leu	Glu	Lys	Met	Gly			
				515					520								525
Leu	Cys	Tyr	Cys	Leu	Asn	Lys	Pro	Lys	Gly	Lys	Pro	Leu	Asn	Gly			
				530					535								540
Ser	Thr	Ala	Trp	Tyr	Lys	Phe	Pro	Cys	Tyr	Val	Gln	Asn	Glu	Val			
				545					550								555
Pro	His	Ala	Glu	Ala	Trp	Ile	Asn	Gly	Thr	Asn	Leu	Ala	Gly	Gln			
				560					565								570
Ser	Phe	Val	Ala	Glu	Gln	Leu	Gln	Ile	Glu	Tyr	Ser	Phe	Pro	Phe			
				575					580								585
Thr	Phe	Pro	Pro	Gly	Leu	Phe	Ala	Arg	Tyr	Ser	Val	Gln	Ile	Asn			
				590					595								600
Ser	His	Val	Val	His	Arg	Ser	Asp	Gly	Lys	Phe	Gln	Ile	Phe	Ala			
				605					610								615
Tyr	Arg	Gly	Lys	Val	Pro	Val	Val	Val	Ser	Tyr	Arg	Pro	Ala	Arg			
				620					625								630
Gly	Val	Leu	Gln	Pro	Asp	Thr	Leu	Ser	Ile	Ala	Ser	His	Ala	Ser			
				635					640								645
Leu	Pro	Asn	Ile	Trp	Thr	Ala	Trp	Gln	Ala	Ile	Thr	Pro	Leu	Val			
				650					655								660
Glu	Glu	Leu	Asn	Val	Leu	Leu	Gln	Glu	Trp	Pro	Gly	Leu	His	Tyr			
				665					670								675
Thr	Val	His	Ile	Leu	Cys	Ser	Lys	Cys	Leu	Lys	Arg	Gly	Ser	Pro			
				680					685								690
Asn	Pro	His	Ala	Phe	Pro	Gly	Glu	Leu	Leu	Ser	Gln	Pro	Arg	Pro			
				695					700								705
Glu	Gly	Val	Ala	Glu	Ile	Ile	Cys	Pro	Lys	Asn	Gly	Ser	Glu	Arg			
				710					715								720
Val	Asn	Val	Ala	Leu	Val	Tyr	Pro	Pro	Thr	Pro	Thr	Val	Ile	Ser			
				725					730								735
Pro	Cys	Ser	Lys	Lys	Asn	Val	Gly	Glu	Lys	His	Arg	Asn	Gln				
				740					745								

&lt;210&gt; 204

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:235708.23.orf1:2002JAN18

&lt;400&gt; 204

Gly	Pro	Arg	Ser	Pro	Leu	Pro	Ile	Leu	Pro	Pro	Ala	Arg	Gly	Ser			
1				5					10					15			
Gly	His	Leu	Met	Ala	Leu	Ala	Gly	Thr	Gln	Val	Gly	Pro	Pro	Pro			
				20					25					30			
Gln	Glu	Arg	Ala	Pro	Glu	Pro	Ile	Gly	Arg	Ala	Trp	Gly	Pro	Pro			
				35					40					45			
Gly	Ile	Thr	Gln	Pro	Ser	Ala	Pro	Gly	Ala	Thr	Val	Gly	Arg	Arg			
				50					55					60			
Val	Ser	Val	Ala	Ala	Gly	Pro	Trp	Leu	His	Gly	Pro	His	Gly	Ser			
				65					70					75			

Cys	Glu	Trp	Val	Arg	Leu	Pro	Gly	Ser	Gly	Asp	Arg	Gln	Arg	Thr	
				80					85					90	
Asp	Pro	Arg	Leu	Gly	Ser	Trp	Arg	Glu	Gly	Arg	Arg	Gly	Ala	Gly	
				95					100					105	
Gln	Pro	Gly	Ser	Asp	Thr	Val	Ser	Ser	Ser	Gly	Arg	Arg	Arg	Pro	
				110					115					120	
Ala	Gly	Ser	Thr	Gln	Ala	Gly	Arg	Gly	Trp	Ala	Ser	Leu	Glu	Pro	
				125					130					135	
Ala	Thr	Ala	Leu	Val	Gly	Thr	Trp	Arg	Arg	Ala	His	Val	Ser	Pro	
				140					145					150	
His	Ala	Ser	His	Arg	Gly	Ala	Leu	Ala	Arg	Arg	Pro	Ala	Arg	Gly	
				155					160					165	
Ala	Cys	Ala	Trp	Asp	Gly	Ser	Gln	Asn	Gln	Arg	Ala	Pro	Val	Arg	
				170					175					180	
Leu	Ala	Ser	Thr	Val	Gly	Leu	Trp	Glu	Ser	Leu	Leu	Phe	Ile	Phe	
				185					190					195	
Lys	His	Leu	Gly	Phe	Ser	Thr	Gly	Ser	Trp	Leu	Leu	Phe	Pro	Gln	
				200					205					210	
Gly	Met	Ser	Leu	Arg	Ser	Arg	Thr	Arg	Trp	Gly	Ser	Gln	Glu	Ala	
				215					220					225	
Ala	Ala	Gln	Ser	Leu	His	Ala	Gly	Lys	Gly	Ser	His	Leu	Ser	Gly	
				230					235					240	
Val	Gly	Ser	Leu	Val	Val	Gln	Gly	Ser	Ala	Gly	Gln	Ser	Leu	Gly	
				245					250					255	
Cys	Ala	Ile	Thr	Ala	Thr	Ala	Phe	Leu	Leu	Gly	Ala	Ser	Thr	Ser	
				260					265					270	
His	Pro	Lys	Thr	Gly	Pro	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Glu	Arg	
				275					280					285	
Thr	Arg	Pro	Arg	Arg	Gln	Gly	Pro	Glu	Tyr	Leu	Gly	Gly	Gly	Asp	
				290					295					300	
Thr	Pro	Arg	Gly	His	Arg	Gly	Gly	Ser	His	Leu	Gly	Thr	Cys	Leu	
				305					310					315	
Leu	Pro	Phe	Ser	Ser	Ser	Ser	Thr	Cys	Gln	Val	Gly	Pro	Trp	Val	
				320					325					330	

&lt;210&gt; 205

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:236649.14.orf1:2002JAN18

&lt;400&gt; 205

Arg	Ala	Trp	Gly	Pro	Leu	Leu	Ser	Ile	Gly	Gly	Gly	Gln	Arg	Gln	
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His	Gln	Arg	Leu	Val	Glu	Gln	Tyr	Arg	Glu	Gln	Ser	Trp	Met	Thr	
				20					25					30	
Met	Ala	Asn	Leu	Glu	Lys	Glu	Leu	Gln	Glu	Met	Glu	Ala	Arg	Tyr	
				35					40					45	
Glu	Lys	Glu	Phe	Gly	Asp	Gly	Ser	Asp	Glu	Asn	Glu	Met	Glu	Glu	
				50					55					60	
His	Glu	Leu	Lys	Asp	Glu	Glu	Asp	Gly	Lys	Asp	Ser	Asp	Glu	Ala	
				65					70					75	
Glu	Asp	Ala	Glu	Leu	Tyr	Asp	Asp	Leu	Tyr	Cys	Pro	Ala	Cys	Asp	
				80					85					90	
Lys	Ser	Phe	Lys	Thr	Glu	Lys	Ala	Met	Lys	Asn	His	Glu	Lys	Ser	
				95					100					105	
Lys	Lys	His	Arg	Glu	Met	Val	Ala	Leu	Leu	Lys	Gln	Gln	Leu	Glu	
				110					115					120	
Glu	Glu	Glu	Glu	Asn	Phe	Ser	Arg	Pro	Gln	Ile	Asp	Glu	Asn	Pro	

125	130	135
Leu Asp Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro Lys Gln		
140	145	150
Lys Leu Ser Lys Lys Gln Lys Lys Lys Lys Gln Lys Pro Ala Gln		
155	160	165
Asn Tyr Asp Asp Asn Phe Asn Val Asn Gly Pro Gly Glu Gly Val		
170	175	180
Lys Val Asp Pro Glu Asp Thr Asn Leu Asn Gln Asp Ser Ala Lys		
185	190	195
Glu Leu Glu Asp Ser Pro Gln Glu Asn Val Ser Val Thr Glu Ile		
200	205	210
Ile Lys Pro Cys Asp Asp Pro Lys Ser Glu Ala Lys Ser Val Pro		
215	220	225
Lys Pro Lys Gly Lys Lys Thr Lys Asp Met Lys Lys Pro Val Arg		
230	235	240
Val Pro Ala Glu Pro Gln Thr Met Ser Val Leu Ile Ser Cys Thr		
245	250	255
Thr Cys His Ser Glu Phe Pro Ser Arg Asn Lys Leu Phe Asp His		
260	265	270
Leu Lys Ala Thr Gly His Ala Arg Ala Pro Ser Ser Ser Ser Leu		
275	280	285
Asn Ser Ala Thr Ser Ser Gln Ser Lys Lys Glu Lys Arg Lys Asn		
290	295	300
Arg		

&lt;210&gt; 206

&lt;211&gt; 213

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:332474.7.orf1:2002JAN18

&lt;400&gt; 206

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Ser Gly Ala Val Pro Ser Ala Ser Val Gly Arg His Pro Leu Ala	
20 25 30	
Ala Glu Pro Ala Leu His Trp Gly Pro Trp Gly Arg Leu Leu Gln	
35 40 45	
Thr Ser Leu Arg Val Val Gly Cys Cys Arg Val Gly Leu Gly Asp	
50 55 60	
Ala Thr Gly Ser Gly Ser Gly Ala Ala Ala Gly Pro Ser Ser His	
65 70 75	
Cys Pro Ser Ser Asp Pro Thr Val Leu Trp Lys Leu Val Gln Gly	
80 85 90	
Thr Cys His Cys Asp His Leu Asp Ala Asp Thr Cys Phe Pro Thr	
95 100 105	
Thr Ala Arg Lys Asn His Gly Pro Gly Ser Leu Ser Phe Gly Asp	
110 115 120	
Val Ala Val Gly Phe Thr Arg Lys Glu Trp Leu Ala Ala Gly Pro	
125 130 135	
Gly Ala Glu Asp Pro Val Pro Gly Cys Asn Ala Gly Glu Leu Gln	
140 145 150	
Pro Pro Ala Leu Cys Gly Leu Asn Cys Leu Leu Ala Trp Lys Ala	
155 160 165	
Gln Leu Ala Gln His Lys Ser Phe Asn Arg Phe Ser Pro Arg Gly	
170 175 180	
Cys Gln Val Ser Lys Pro Ala Val Ile Ser Ser Leu Glu Gln Gly	
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Pro Glu Ser                    200                    205                    210

<210> 207  
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 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte ID No: LG:335727.8.orf2:2002JAN18

<400> 207  
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           20                  25                  30  
 Ile Gly Cys Thr Met Ser Ala Phe Glu Lys Pro Gln Ile Ile Ala  
           35                  40                  45  
 His Ile Gln Lys Gly Phe Asn Tyr Thr Val Phe Asp Cys Lys Trp  
           50                  55                  60  
 Val Pro Cys Ser Ala Lys Phe Val Thr Met Gly Asn Phe Ala Arg  
           65                  70                  75  
 Gly Thr Gly Val Ile Gln Leu Tyr Glu Ile Gln His Gly Asp Leu  
           80                  85                  90  
 Lys Leu Leu Arg Glu Ile Glu Lys Ala Lys Pro Ile Lys Cys Gly  
           95                  100                 105  
 Thr Phe Gly Ala Thr Ser Leu Gln Gln Arg Tyr Leu Ala Thr Gly  
          110                 115                 120  
 Asp Phe Gly Gly Asn Leu His Ile Trp Asn Leu Glu Ala Pro Glu  
          125                 130                 135  
 Met Pro Val Tyr Ser Val Lys Gly His Lys Glu Ile Ile Asn Ala  
          140                 145                 150  
 Ile Asp Gly Ile Gly Gly Leu Gly Ile Gly Glu Gly Ala Pro Glu  
          155                 160                 165  
 Ile Val Thr Gly Ser Arg Asp Gly Thr Val Lys Val Trp Asp Pro  
          170                 175                 180  
 Arg Gln Lys Asp Asp Pro Val Ala Asn Met Glu Pro Val Gln Gly  
          185                 190                 195  
 Glu Asn Lys Arg Asp Cys Trp Thr Val Ala Phe Gly Asn Ala Tyr  
          200                 205                 210  
 Asn Gln Glu Glu Arg Val Val Cys Ala Gly Tyr Asp Asn Gly Asp  
          215                 220                 225  
 Ile Lys Leu Phe Asp Leu Arg Asn Met Ala Leu Arg Trp Glu Thr  
          230                 235                 240  
 Asn Ile Lys Asn Gly Val Cys Ser Leu Glu Phe Asp Arg Lys Asp  
          245                 250                 255  
 Ile Ser Met Asn Lys Leu Val Ala Thr Ser Leu Glu Gly Lys Phe  
          260                 265                 270  
 His Val Phe Asp Met Arg Thr Gln His Pro Thr Lys Gly Phe Ala  
          275                 280                 285  
 Ser Val Ser Glu Lys Ala His Lys Ser Thr Val Trp Gln Val Arg  
          290                 295                 300  
 His Leu Pro Gln Asn Arg Glu Leu Phe Leu Thr Ala Gly Gly Ala  
          305                 310                 315  
 Gly Gly Leu His Leu Trp Lys  
                   320

<210> 208  
 <211> 238  
 <212> PRT  
 <213> Homo sapiens



&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: LG:481983.1.orf3:2002JAN18

&lt;400&gt; 208

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Thr	Thr	Asn	His	Ser	Phe	Phe	Phe	Phe	His	Leu	Gln	Pro	Leu	Thr	20	25	30	35
Thr	Asp	Leu	His	Tyr	Tyr	Ile	Leu	Glu	Leu	Ser	Phe	Tyr	Trp		40	45	50	55
Ser	Leu	Met	Phe	Ser	Gln	Phe	Thr	Asp	Ile	Lys	Arg	Lys	Asp	Phe	60	65	70	75
Gly	Ile	Met	Phe	Leu	His	His	Leu	Val	Ser	Ile	Phe	Leu	Ile	Thr	80	85	90	95
Phe	Ser	Tyr	Val	Asn	Met	Ala	Arg	Val	Gly	Thr	Leu	Val	Leu		100	105	110	115
Cys	Leu	His	Asp	Ser	Ala	Asp	Ala	Leu	Leu	Glu	Ala	Ala	Lys	Met	120	125	130	135
Ala	Asn	Tyr	Ala	Lys	Phe	Gln	Lys	Met	Cys	Asp	Leu	Leu	Phe	Val	140	145	150	155
Met	Phe	Ala	Val	Val	Phe	Ile	Thr	Thr	Arg	Leu	Gly	Ile	Phe	Pro	160	165	170	175
Leu	Trp	Val	Leu	Asn	Thr	Thr	Leu	Phe	Glu	Ser	Trp	Glu	Ile	Val	180	185	190	195
Gly	Pro	Tyr	Pro	Ser	Trp	Trp	Val	Phe	Asn	Leu	Leu	Leu	Leu	Leu	200	205	210	215
Val	Gln	Gly	Leu	Asn	Cys	Phe	Trp	Ser	Tyr	Leu	Ile	Val	Lys	Ile	220	225	230	235
Ala	Cys	Lys	Ala	Val	Ser	Arg	Gly	Lys	Ala	Gly	Lys	Trp	Asn	Pro				
Tyr	Met	Cys	Pro	Arg	Met	Ile	Glu	Val	Ile	Leu	Ser	Leu	Ala	Gln				
Met	Arg	Arg	Thr	Gln	Asn	Leu	Arg	Glu	Arg	Ile	Pro	Thr	Leu	Arg				
Gln	Pro	Pro	Met	Gly	Pro	Val	Val	Pro	Thr	Gly	Ile	Ser						



(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
31 July 2003 (31.07.2003)

PCT

(10) International Publication Number  
**WO 2003/062379 A3**

(51) International Patent Classification<sup>7</sup>: **C12N 15/11**,  
15/12, 15/00, C12Q 1/68, C07K 14/00, 14/435

(21) International Application Number:  
PCT/US2003/001363

(22) International Filing Date: 14 January 2003 (14.01.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
60/349,946 17 January 2002 (17.01.2002) US  
60/349,413 17 January 2002 (17.01.2002) US

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published:**

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:  
19 February 2004

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: MOLECULES FOR DISEASE DETECTION AND TREATMENT

(57) Abstract: The present invention provides purified disease detection and treatment molecule polynucleotides (mddt). Also encompassed are the polypeptides (MDDT) encoded by mddt. The invention also provides for the use of mddt, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing mddt for the expression of MDDT. The invention additionally provides for the use of isolated and purified MDDT to induce antibodies and to screen libraries of compounds and the use of anti-MDDT antibodies in diagnostic assays. Also provided are microarrays containing mddt and methods of use.

WO 2003/062379 A3

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/01363

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) : C12N 15/11, 15/12, 15/00; C12Q 1/68; C07K 14/00, 14/435  
US CL : 536/23.1, 23.5; 435/6, 320/1, 325, 252.3; 530/350; 514/12

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 23.5; 435/6, 320/1, 325, 252.3; 530/350; 514/12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
Compugen, SEQ ID NOs: 1 and 105

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01/53312 A1 (HYSEQ, INC.) 26 July 2001 (26.07.2001), compare SEQ ID NO: 1, position 529-1305 to reference SEQ ID NO: 1215, positions 403-1179 and see alignment attached to the reference.	3 and 6-8
Y		16 and 20-26
X	EP 1033401 A2 (GENSET) 06 September 2000 (06.09.2000), compare SEQ ID NO: 105, positions 25-140 to SEQ ID NO: 7103, positions 1-116 and alignment attached to reference.	27

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 26 August 2003 (26.08.2003)	Date of mailing of the international search report <b>05 DEC 2003</b>
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No.	Authorized officer James Martinell <i>[Signature]</i> Telephone No. (703) 308-0196 <i>[Signature]</i>

Form PCT/ISA/210 (second sheet) (July 1998)

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/01363

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: Please See Continuation Sheet
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☒  
☐

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

INTERNATIONAL SEARCH REPORT

PCT/US03/01363

**Continuation of Box II Item 3:**

1-10, 12, 13, 16, 17, and 19-28 to the extent that they include SEQ ID NO: 1 and 105

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